11, Appl 63, Appl 12, Appl 12, Appl 64, Appl 11, Appl

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Sequence 2

Seguence Sequence Sequence 1, Appli Sequence 3, Appli Sequence 404, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 24, Appli Gence 24, Appli Thence 24, Appli Thence 28, Appli Thence 29, Appli

Seguence Sequence Sequence

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Sequence 13, Application US/08948564
Patent No. 6121512
GENERAL INFORMATION:
APPLICANT: Siminszky, Balazs
APPLICANT: Devey, Ralph E.
APPLICANT: Devey, Ralph E.
APPLICANT: OCTDIN, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
US-09-059-769-20
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-948-564-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Benett, Vitaginia C.
REGISTRATION NUMBER: 37.092
REFERENCE/DOCKET NUMBER: 5051-409
TELEPHONE: 919-854-1400
TELEPHONE: 919-854-1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Virginia C. Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
COUNTRY: USA
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INFORMATION FOR SEQ ID NO:
SEPOITENCE CHARACTERISTICS:
                                                     CLASSIFICATION:
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-MODEL=frame+p2n.model-DEV=xlh
-D=122.J/USPTG_SPOOL/USO985781/runat_27052003_150658_10345/app_query.fasta_1.711
-DB=158.ued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRRT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THE_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -ALIGN=15
-NORM=COCALIGN=200 -NORM=ext -HBAPSIZE=500 -MINLEN=0 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-ICPU=30 -THREDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
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              GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-292-768-67
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                                                                                       IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys
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GENERAL INFORMATION:
APPLICANT: BOUNG-JUN, OH
APPLICANT: WOUNG SOON KIM
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN T TITLE OF INVENTION: A LOWARTHBLE INTERACTION
FILE REFERENCE: 10324/P644310SO
CURRENT APPLICATION NUMBER: US/09/499;302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 1781
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        pairs
LENGTH: 1824 base pair.
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
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; LOCATION:
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Matches:
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ORGANISM: Capsicum annuum
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Query Match:
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US-09-499-302A-1
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323 AsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp*** 342
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                                                    343 LeuvalAspGluvalAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThr
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APPLICANT: Croteau, Rodney B.
APPLICANT: Lupien, Shari L.
APPLICANT: KATP, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXXLASES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
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1420 Fifth Avenue, Suite 2800
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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APPLICATION NUMBER: US/08/881,784
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REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: WST
TELECOMMUNICATION INFORMATION:
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NAME: Shelton, Dennis K.
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       623 ITGCTGAAGGAGTCGCTGGCATTGGCGTCCGGGTTTGAGCTGGCGGAT---CTCTACCCT 679
                                                                              TCCTCATGGCTCCTCAACCTGCTTAGCTTGAACAAGTAC-----AGGTTGCAGAGGATG 733
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Patent No. 6194185

GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION (TITLE OF INVENTION: LIMONENE HYDROXYLASES)
FILE REFERENCE: wsur13463
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                                             ---LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle
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LOCATION: 558..1212
OTHER INFORMATION: /product=
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; LOCATION: 39..538
; OTHER INFORMATION: /product=
TELEFAN: (206) 224-0719
TELEFAN: (206) 224-0779
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1762 base pairs
TYPE: nucleic acid
STRANDENBES: single
TOPOLOGY: linear
                                                                                                                                              MOLECULE TYPE: CONA
ORIGINAL SOURCE:
ORGANISM: Mentha spicata
INDIVIDUAL ISOLATE: CDNA er
IMMEDIATE SOURCE:
CLONE: PSM12.2
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CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SSOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 1762
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ORGANISM: Mentha spicata
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LOCATION: (20)..(1507)
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                                                                                                                                                                                                                                             GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
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APPLICANT: Croteau, Rodney B
APPLICANT: LUDien, Shari L
APPLICANT: LUDIen, Shari L
APPLICANT: LUDIEN
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE PEPERENCE: Wairi3463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT APPLICATION NUMBER: US/09/292,768
EARLIER REPERCATION NUMBER: 08/881,784
EARLIER PILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 65
                                                             GAGAAGAAGAGCGGCGAGTTTGGAGGCCAAGGACATCGTCGACGTT
                                                                                                                                                                            CTITICAGGATGCAGAAGGCCAGCGACATCAAATTCCCATTACTTCCAATTGCATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle
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                                                                                                                                                                                                                                                                                                          GGTTTCATTTTCGACACCTTCTCCGCGGGAGCTGAAACGTCTTCGACGACCATCTCATGG
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                                                                                                                   LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys******IleLys
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GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
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                                                                                                                                                                                          GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp
                                                                                                                                                                                                                                                    GGTTTCATTTTCGACACCCTTCTCCGCGGGAGCTGAAACGTCTTCGACGACCATCTCATGG
                                                                                                                                                                                                                                                                                                              316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr
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LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLys
                                                                                                                                      CTTTTCAGGATGCAGAAGGGCAGCGACATCAAAATTCCCATTACTTCCAATTGCATCAAG
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APPLICANT: Croteau, Rodney B.
APPLICANT: Lupien, Shari L.
APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
NUMBER OF SEQUENCE: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
ADDRESSEE: PLLC
STREET: 1420 Fifth Avenue, Suite 2800
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: computer-generated nucleic acid sequence encoding OTHER INFORMATION: limonene-6-hydroxylase
                                                                                                                                                                                             encoding
                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)..(1762)
OTHER INFORMATION: computer-generated nucleic acid sequence
OTHER INFORMATION: spearmint limonene-6-hydroxylase variant
FEATURE:
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Mismatches:
Indels:
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Matches:
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-09-292-768-65
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Best Local Similarity:
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APPLICANT: Croteeu, Rodney B
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                             910 ACGTICTCAGCGGGGACCGAGACATCATCACCACCACCTGTGGTGATGGCGGAGCTG 969
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            TCGGGGTTCGAGCTCGCCGACATGTTCCCCTCCTCCAGCTCCTCAACTTGCTCTGCTGG 717
                                                                                                                                                                                                   262 Glu******GluGlyGlu***SerGlyVal---***LeuAspThrLeuLeuGluPheAla 280
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                                                            -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAsp
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Conservative:
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Indels:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,784
FILING DATE:
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: WSUR1977
REFERENCE/DOCKET NUMBER: WSUR1977
TELEPHONE: (206) 224-0718
TELEFAK: (206) 224-0719
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1665 base pairs
TYPE: nucleic acid
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Best Local Similarity:
Query Match:
DB:
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GENERAL INFORMATION:
APPLICATY: Croteau, Rodney B
APPLICATY: Croteau, Rodney B
APPLICATY: Croteau, Redney B
APPLICATY: Croteau, Recombinant Materials and Methods for the Production of TITLE OF INVENTION: LEGORINAME HYDROXYLASES
TITLE OF INVENTION: LIMONENE HYDROXYLASES
TITLE OF INVENTION: LIMONENE HYDROXYLASES
TITLE REPRESENCE: Washridd
CORRENT APPLICATION NUMBER: 08/081,784
EARLIER APPLICATION NUMBER: 08/081,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
LENGTH: 1665
TYPE: DNA
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970 ATGAGGAATCCAGAGGTGATGGCGAAAGGGGGAAAGGGGG 1029
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                         Glu******GluGlyGlu***SerGlyVal---***LeuAspThrLeuLeuGluPheAla 280
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; Sequence 67, Application US/09292768
; Patent No. 6194185
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                       US/09/292,768
                 CURRENT APPLICATION NUMBER: US/09/292, CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
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FILE REFERENCE: wsur13463
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; LOCATION: (19)..(1518)
US-09-292-768-3
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              FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase
                                                               FEATURE:
NAME/KEX: misc_feature
LOCATION: (1): (1665)
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase variant
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ORGANISM: Artificial Seguence
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NAME/KEY: CDS

LOCATION: (19)..(1518)

US-09-292-768-67
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APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Karp, Frank
TITLE OF INVENTION: ERCOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: wan13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT PEPLICATION NUMBER: 08/09/292,768
EARLIER APPLICATION NUMBER: 08/08/14
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 659
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                                                                                                                                   GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp
                                                                                                                                                                                                       850 AAGGATAGCCAGATCAAAGTCCCCATCACCACAAAGCCATCAAAGCCTTCATCTTCGAC
                                                                                                                                                                                                                                                                                  ***Pheseralagly***AspserThrala*****ThrGluTrpalaLeuAlaGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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-LeuGlyPro

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--TCCGATATGGACATGTCTGAGGCAGAAGGCCTT 1461
281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp
                                                                                                                                                                                                                                                GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys
                                                                                                                                                                                                                                                                                                                                                                                                        309 CCATTIGGAGCTGGAAGAATCTGCCCCGGTTTGAATTTCGGGTTGGCAAATGTTGAG
                                                                                                AAGGATAGCCAGATCAAAGTCCCCATCACCACCAACGCCATCAAAGCCTTCATCTTCGAC
                                                                                                                                    ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu
                                                                                                                                                                           910 ACGITCICAGCGGGACCGAGACAICATCAACCACCACCIGIGGGIGAIGGCGGAGCIG
                                                                                                                                                                                                                    IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys
                                                                                                                                                                                                                                                                                                 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys
                                                                                                                                                                                                                                                                                                                                        1030 AAGACGGACTGGGACGTGGACGACGTGCAGGAGCTTAAGTACATGAAATCGGTGGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1210 GGTAGGAATCCTCTCTACTGGGAAAAACCCGGAGACCTTTTGGCCCGAAAGGTTT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu
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Patent No. 6380465;
GENERAL INFORMATION:
TITLE OF INVENTION: Cytochrome P450 Enzymes;
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
FILE REFERENCE: P-1049
CURRENT APPLICATION NUMBER: US/09/351,229
CURRENT FILING DATE: 1999-07-11
EARLIER FILING DATE: 1998-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIN Ver. 2.0
SSC ID NO 3
LENGTH: 1806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ******GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GlualaGluGluIleArgAspIleAlaArgGluValLeuLysIle*** 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glu******GluGlyGlu***SerGlyVal---***LeuAspThrLeuLeuGluPheAla 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIGGIGGAC --- CCGGCCTGCGCGGACCGGTTCGAGAGCATCGGGACGAAGATCATGTGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIGCCGCACCACGCCACCAGCGIGGCCAAGCAGIACGCCCAGTGGCGCACGIGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CTCGGCGAGGTGTTCTCCGTCGTCGTCCTCCGCGAGGCCCACGAGGAGGCGATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||||
TACGACAACGACGACATCTTCAGCCCTACAGCGTGCACTGGCGCCAGAGTGCGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCTCACGGAGCGGATAGCGACGCTGACGTGCTCCATCATCTGCAGGGCGGCGTTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer*****
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCTGCGTCTCCGAGCTCCTCAGCGCCCGCAACGTCCGCTTCCGGCTTCATCAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 598 AGCGIGATCAGGGACCACGAGGAGCIGGIGGAGCIGGIGAAGGACGCCCTCAGCATGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProvalvalGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly
        OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase
                                                                                                                              OTHER INFORMATION: computer-generated nucleic acid sequence OTHER INFORMATION: limonene-3-hydroxylase protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGluTyrSerLeuThrAspPhelle***ProLeuLys***Leu----
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147
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Matches:
Conservative:
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48.178
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26.158
                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1665)
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LOCATION: (19)..(1518)

US-09-292-768-69
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Best Local Similarity:
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Best Lo Query M DB:	Local Similarity: 29.35% Mismatches: 213 / Match: 25.77% Indels: 41	99 3
-06	x US-09-172-339-5 (1-1762)	н
Qy	ProAsnProProSerPro*	,
අුධ	101 TCGAAATCCCAACAAAACTACTTCCGAGCCCTCCGAAGCTGCCGGTGATC 151	П
Qy	46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65	Oy . 3
qa	152 GGCCACCTCCACTTCTGGGGGGGGGCTTCCCCAGCACGTGTTTAGGAGCATAGCCCAG 211	an
Qy	LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr	CY 4 Db 12
qq	212 AAGTACGGGCCGGTGGCGCACGTGCGAGAGAGTGTACTCGGTGGTGCTGTCGTCG 271	
Q.y	<pre>6 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe**ThrArgPhe                                      </pre>	da
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λο 7	06 GlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla****Pro***	
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QY		RESULT 13 US-09-292-7
qa		; Sequence ; Patent No
. ΟΥ	185 SerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200	GENERAL I APPLICAN
qq	563 GTCGTCGTGTGCAGGGCGGCGTTCGGGAGTGTGCTCAAGGACCAGGGTTCGTTGGGGGAG 622	, APPLICAN
Qy	201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220	TITLE OF TIT
Dp	623 TIGGIGAAGGAGICGCIGGCATIGGCGICCGGGITIGAGCIGGCGGAICICTACCCI 679	CURRENT
Qy Db	221	CONNENT ; EARLIER ; NUMBER O
QY	237 LeuAsnLysPheAspProValValGluArgVallleLysLysArgArg***IleValArg 256	; SOFTWARE ; SEQ ID NO
QQ	734 CGCCGCCGCCTCGATCATCCTTGATGGGTTCCTGGAGGAGCATAGG781 .	, LENGTH: , TYPE: D
QY	257 ArgArg***AsnGlyGlu******GluGlyGlu***SerGlyVal***LeuAspThr 275	; ORGANISI ; FEATURE
qq	TTGGAGGCGAGGACATCGTO	LOCATIO
ΟŸ	276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys******11eLys 295	US-09-292-7
qq	827 CITICAGGAIGCAGCCGGGCAGCGACAGCAAAITCCCATTACITCCAATIGCATCAAG 886	
Qy	296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315	Score: Percent Sim
qq	887 GGTITCATITICGACACCTICTCCGGGGAGCTGAAACGICTICGACGACCAICTCAIGG 946	Query Match
QY	316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu**Tyr 335	118-09-857-5
qa		
Qy	336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355	27 Db 1
qq	1007 GAGGCGCTCAAGGGAAAGACAGTCGTGGATTTGAGCGAGGTGCAAGAGCTAAAATACCTG 1066	!

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ANT: Croteau, Rodney B
ANT: Croteau, Rodney B
ANT: Croteau, Rodney B
ANT: Lupien, Shari L
ANT: Karp, Frank
OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
OF INVENTION: LIMONENE HYDROXYLASES
TERRENCE: Wall 143
T FILING DATE: 1999-04-14
R APPLICATION NUMBER: 08/881,784
R APPLICATION NUMBER: 08/881,784
R RILING DATE: 1997-06-24
: OF SEQ ID NOS: 70
RE: Patentin Ver. 2.0
                                                                                                                                     396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***Argpro 415
                                                                 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
                                                                                                                                                                                                         416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
                                                                                                                                                                                                                                                                                                                                                                                                                    476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
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Matches:
Conservative:
Mismatches:
Indels:
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5, Application US/09292768
0. 6194185
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611.50
47.86%
30.55%
25.52%
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ION: (1)..(1494)
-768-5
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| Similarity;
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1180 TCCATGGGCAGGAATCCTCTACTGGGAAAACCGGATACCTTTTGGCCCGAAAGGTTT 1239  Qy 419 LeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln 438  1240		MELLUM TYPE: I LOPPY GIRE  COMPUTER: IEM PC COMPATIBLE  COMPUTER: IEM PC COMPATIBLE  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  FILING DATE: CLASSIFICATION: 800  ATYONEV/AGENT INDORMATION:  NAME: Bennett, Vigginia C.  REGISTRATION NUMBER: 37,092  REDERGNEW/ACTION INDORMATION:  TELEPAN: 919-854-1400  TELEPAN: 919-854-1401  INFORMATION FOR SEQ ID NO: 11:  SEQUENCE CHARACTERISTICS: LENGTH: 1657 base pairs  TYPE: nucleic acid  STRNDEDDESS: single  TOPELOGY: linear  MOLECULE TYPE: CDN  REALTOR: 1.1548  US-08-948-564-11  Alliqument Scores: 3.57e-69  Percent Similarity: 46.03% Conservative: 99  Percent Similarity: 46.03%
55 LeuLeuHisTyrala***IleAspLeuSerLysLysHisGlyproLeuPheSer***** 74  11	460 GACGAGGTGTCGCCCCCCCCCCCCTCTTCGGCAGGGGGCGCCGTG 513  174 ASP**ThrGluGluLeuLeuLySTrp**ASnSerThr**SerMetMet***LeuGly 193  184 GACATGACGGACAGGATGACGTGCTCCATCATCATCTGCAGGCGCGTTCGG 573  194 GluAlaGluGluIleArgAsp	Asnalyglu******dluGlyGlu***SerGlyVal**LeuAspThrLeuLeuGlu 27

Oy 312 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArg 331  Db 970 ACAATAGTTTGGGCAATGAATGCACTGTTGAGAATCCCAATGTGAGCAAGGTTCAA 1029	Qy 332 GluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsn 351	Qy 352 LeuProTyrIleArgalaIleValLysGluThrPheArgMetHisProProLeuPro 370	Oy 371 ValValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGly 390 :::::	Oy 391 AlaLeu*****PheasnValTrpGlnValGly***Asp***LysTyrTrpAspArgPro 410 :::	<pre>411 SerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****Leu 43</pre>	Oy 431 AspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCys 449 :::   :::	0 Pr 9 CC	Oy 470 PheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488	489Val ::: 1468 ATGTTG	Oy 508 Val 508 	RESULT 15 US-08-606-505B-63 Sequence 63, Application US/08606505B ; Patent No. 6114601	GENERAL INFORMATION: APPLICANT: KIKOCHI, Yasuhiro APPLICANT: KIYOKAWA, Shiqeto APPLICANT: SHIMADA, Yukihisa	; APPLICANT: OHBAYASHI, Masaya ; APPLICANT: SHIMADA, Ritsuko ; APPLICANT: OKINAKA, Yasushi ; TITLE OF INVENTION: NOVEL PLANT GENES	HUMBER OF SEQUENCES: 67 CORRESPONDENCE ADDRESS: ADDRESSES: FITZPATRICK, CELLA, HARPER & SCINTO STRRET: 30 ROCKEELLET Plaza		COMPUTER READABLE FORM:  HOBIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.  COMPUTER: IBM FS/V.  OPERATING SYSTEM: MS-DOS Ver3.30	PATENT AID Ver1.0 ICATION DATA: NN NUMBER: US/08/606, E: 23-MAR-1996
Best Local Similarity:       27.73%       Mismatches:       22         Query Match:       34.62%       Indels:       70         DB:       3       Gaps:       15         US-09-857-581-66 (1-521)       x US-08-948-564-11 (1-1657)       1657)	2 LeuLeugluLeualaLeuglyLeu***ValLeual 	**Pro 4	la*** GCCTA	roThr        AAACC	ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******CluAlaThrSer 	Oy 101 Phe***ThrargPheGlnThrSerAla***Arg***LeuThrTyrAsp*****Val 119   1	spleu 1         ACCIC 3	Qy 140 LeuAsnAlaThrThalAsn***LeuArgProLeuArgThrGlnGln1leArgLys*** 159	Cy 160 Leuarg***MetalaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179 :::::	Qy 180 LeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGlu 194 ::: ::           520 ATGICTTTCACGAACTCTTTGATATGCAGAATCGCGTTGGGGAAAAGTTACGGTTGTAG 579	spile ::: TTCTG	<pre>Qy 202 AlaargGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeu 221</pre>	Oy 222 Lys***LeuLysValGlyLysTyrGluLysArglleAspAspIleLeuAsnLysPheAsp 241 :::       :::::	Oy 242 ProValValGluArgValIleLySLySArgArg***IleValArgArgArg4**AsnGly 261	Oy 262 Glu*****GluGlyGlu***SerGlyVal	QY 272 ***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLySIleThrLyS 291 :::	Oy 292 *****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrala*** 311        :::::::::

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1271 AGGCTCAGCGTTAACATATGGGCTATTGGAAGAGATCCATCTGTGTGGGAAAATCCAAAT 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1439 ACAAGATTGGGAATACTTCTAGTGGAGTATATTTTGGGAACTTTGGTGCATTCTTTTGTT 11498
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                                             -GlyGluAlaGluGluIleArgAspIleAlaArg
                                                                                                                                              LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys***
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 Leu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSer
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                                                                                 671 AGCAAGCGAGTTTTCGGGTCTCAAGGATCAGAATCCAATGAGTTCAAAGATATGGTGGTT
                                                                                                                                                                                                                                                                                                                                                 -***AsnGlyGlu******GluGlyGlu***SerGlyVal***
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                                                                                                                                                                                                                                                                                                           851 TTGACTCGGTTGCTGGAAGAGCACACTGCATCGGCTCATGAGCGTAAAGGCAGCCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ***IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****
                                                                                                                       GluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***
                                                                                                                                                                                                                                                                      ValGluArgValIleLysLysArgArg***IleValArgArgArg-----
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                                                                                                                                                                                                                                                                                                                                                                                   TTCCTTGATTTTGTCGTTGCAAATGCCGACAATTCTGAAGGCGAA------
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Job time : 97 secs
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152
97
222.
69
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP44963/92
FILING DATE: 02-MAR-1992
ATTORNEY, AGENT INFORMATION:
NAME: PEITY, LAWIENCES.
REGISTRATION NUMBER: 31865
TELEPHONE: 212-218-210
TELEPHONE: 212-218-220
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 2174 base pairs
                                                                                                                                                                                                                              LENGTH: 2174 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
NOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: Eustoma russellianum
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582.50
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24.31%
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Best Local Similarity:
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Sequence 1997, Apple Sequence 3, Appli Sequence 1506, Apple Sequence 15, Appli Sequence 212, Appli Sequence 22, Appli Sequence 53, Appli

Sequence 2669. Applementer 2172, Applementer 2172, Applementer 2172, Applementer 2174, Applementer 2174, Applementer 2177, Applementer 2177, Applementer 2177, Applementer 2177, Applementer 2177, Applementer 2173, Applementer 2174, Applementer 217

Run on:

Title:

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APPLICANT: ALGO, YUNG
APPLICANT: ALGO, YUNG
APPLICANT: ALGO, YUNG
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
US-09-814-786-1
US-09-938-842A-1997
US-09-947-027-3
US-10-001-009-3
US-09-938-842A-1506
US-10-142-231-55
US-10-067-534-1
US-09-938-842A-2124
US-09-938-842A-2124
US-09-938-842A-2124
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US-10-142-231-53
US-09-938-842A-2669
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US-09-938-842A-1189
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US-09-938-842A-1188
US-09-938-842A-1479
US-09-938-842A-1479
US-09-938-842A-1382
US-09-931-267-3
US-09-931-267-3
US-09-931-267-3
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US-09-349-385-9
US-09-938-842A-1300
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US-09-770-445-543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1009, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana
  APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
  US-09-938-842A-1009
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  TYPE: DNA
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Sequence 199, App
Sequence 63, Appl
Sequence 64, Appl
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US-09-9814-786-63
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuq
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Sequence 1, Appli Sequence 835, App Sequence 9, Appli Sequence 1300, Ap

Sequence 2, Appli Sequence 795, App Sequence 543, App

0y 337 ValValGIyLysAsp***LeuValAspGluValAspThrGInAsnLeuProTyrIlearg 356	Oy 397 ValTrpGlnValGly***Asp**LysTyrTrpAspArgProserGlu***ArgProGlu 416  1210 TCTTATGCTATGAGAGATCCTGATTCATGGGAAGATCCTGATGAGTTTAAACCAGAG 1269  Oy 417 ArgPheLeuGluThr***AlaGluGlyGluAla****LeuAspLeuArgGly***His 436  1270 AGGTTCTAGGTAGGAGAGAGAGAGAGAGAGAATCTGAGAAAATC 1317  Oy 437 PheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThr 456  11111111111111111111111111111111111	Qy 457 SerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGly 476  1378 ATATTGTAGGAACGGCATTGGGATGATGATGATGATTGACTGGAATCAATGGA 1437  Qy 477 ProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495  Db 1438 GACAAGATTAATATGGAAGGCTACTGGA 1467  Qy 496 GlyLeuThrValProArgAlaHisSerLeuValScyValProLeuAlaArgIleGlyVal 515	Db 1468 GGTTTCTCATCACCATGGCTTACATGCACTCCTATTCCTCTTCCCCGAACC 1527  Qy 516 AlaSerLysLeuleuSer 521  Db 1528 CAAAACTCTTAATTCC 1545	O EA	TIE OF INVENTION: STATES TECOLATED GENES OF PLANTS, INANSCENIC PLANTS  LE REPRENCE: SCR.P1300-3  RRENT APPLICATION NUMBER: US/09/938,842A  RRENT FILING DATE: 2000-08-24  IOR APPLICATION NUMBER: US 60/227,866  IOR APPLICATION NUMBER: US 60/264,647  IOR APPLICATION NUMBER: US 60/264,647  IOR PILING DATE: 2001-01-16  IOR APPLICATION NUMBER: US 60/300,111  IOR APPLICATION NUMBER: US 60/300,111  IOR PILING DATE: 2001-06-22  MBER OF SEQ. ID NOS: 5379  ID NO 199  ID NO 199	; TYPE DNA ; ORGANISM: Arabidopsis thaliana US-09-938-842A-199 Aliqument Scores: 4.23e-77 Length: 1539 Score: 593.50 Matches: 153 Percent Similarity: 29.59% Mismatches: 224 Query Match: 24.77% Indels: 41
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	0y 418 pheleuGluThr***AlaGluGlyGluAla*****LeuAspleuArgGly***HisPhe 437   1	786 co co sa ya ya co	MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage. COMPOTER: IBM PSA'V OPERATING SYSTEM: MS-DOS Ver3.30 SOFTWARE: PATENT AID Ver1.0 CURRENT APPLICATION DATA: APPLICATION NOWBER: US/09/814,786 FILING DATE: 23-MAI-2001 PRIOR APPLICATION DATE: APPLICATION DATE: US/09/616,990 FILING DATE: 14-Jul-2000 APPLICATION NUMBER: US/09/616,990 FILING DATE: 14-Jul-2000 APPLICATION NUMBER: US/09/616,990 FILING DATE: WARRINGER: US/09/616,990 FILING DATE: US/09/616,990
Gaps:  14  66 (1-521) x US-09-938-842A-199 (1-1539)  LeualaLeuphe***HisLeuArgProThrPro***Ala***SerLySAlaLeuArgHis 31  :::	Ser*****PheGlySerMetProThrValValalaSerThrProGluLeuPheLysLeu 91	AsnSer 18 ::::: TCAAAC 57 Argasp 20 :::    CAAGAC 63 ***PFO 22 CCATTT 69 CCATTT 69 LysPhe 24 AGATTG 75 Argarg 25 Argarg 25	***AsnGlyGlu******GluGlyGlu****SerGlyVal***LeuaspThrLeuLeuGlu 278 ::::::::::::::::::::::::::::::::::::
DB:  US-09-857-581-66 (1-521) x US-09-938-842A-199 (1-1539)  QY	72 Ser*****PheGlySerMetProThrValValAlaSerThrProGluLeuPhel		259 ***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuaspThrLeu  1. :: :: :: ::: ::: ::: ::: ::: ::: :::

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   GAGTTGATGACTGTTGCTGGCTATTTCAACATAGGTGATTTTATCCCCTCGATTGCATGG 790
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|GAAATGGACGGTGTGATCGGCCGAGACCGGCGGTTTCTTGAGGCAGACATATCAAAGTTG
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                                       LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVal
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SHIMADA, Yukihisa
OHBAYASHI, Masaya
SHIMADA, Ritsuko
OKINAKA, Yasushi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTTCTTTCATGTGCAAAACTTGTGCAATATCTATGGATGAATTCCAGGCGCCACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCCACCTGGCCCGATA - - - GGGTGGCCGGTTCTCGGTGCCCTTCGGCTTTTA - - - GGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysLeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ***PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAACACTIGAC---AIGAACTICICGAAICGGCCGCCIAAIGCAGGGGCIACCATIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTATAATGCTCAGGACATGGTGTTTGCAGACTATGGTCCCAGATGGAAGCTGCTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLeulleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACTCAGCAACATACACATTCTTGGTGGCAAGGCCCTGCAGGGCTGGGAAGAAGTTCGA
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152
97
222
69
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-857-581-66 (1-521) x US-09-814-786-63 (1-2174)
                                                                                                                                                                                                                                      IDENTIFICATION METHOD: by experiment SEQUENCE DESCRIPTION: SEQ ID NO: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetLeuLeuGluLeuAlaLeuGlyLeu***Val-
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                  ORGANISM: Eustoma russellianum
INFORMATION FOR SEQ ID NO: 63 :
SEQUENCE CHARACTERISTICS:
LENGTH: 2174 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 92 to 1621
IDENTIFICATION METHOD:
                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA ORIGINAL SOURCE.
                                                                                                                                                                                                                                                                                                                          3.03e-75
582.50
46.11%
28.15%
24.31%
                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                               ----***SerMetMet** 191
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                          largLysLeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArqProLe 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 TGTAAATGTTAAGGCACTTCTTTTTGGATTTATTCACGGCGGGCACGGATACATCATCAAG
                                                                 578 GCGAAAGCTATGTAGCTTGCACATGTTAGGCCCGAAGGCACTCGAGGATTGGGCTCATGT
                                                                                                           uArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***Ly
                                                                                                                                                                                                                                       698 GCCAGTGCCAGTGGTGCCAGAGATGTTAACTTATGCCATGGCTAATATGATTGGACG
                                                                                                                                                                                                                                                                                                                          758 AATCATACTCAGCCGACGCCCTTTTGTTATCACGAGCAAATTAGACTCGTCTTCTGC
                                                                                                                                                                                                                                                                                                                                                                   *LeuGlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGl
                                                                                                                                                                                                                                                                                                                                                                                                       818 ITCTGCTTCTGTTAGTGAATTCCAATATAGGTTATGGAGCTCATGAGGATGGCAGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 uTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sArglleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 gArg***IleValArgArgArg***AsnGlyGlu******GluGlyGlu***SerGlyVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 1***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1035 -TTTCTTGATATTCTTATGGCGGCTACCCAAGAAACACGGGGGGAATTCAGCTTAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 gGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1274 CTTGCCATATTTCCAAGCCATATGCAAAGAACATTCCGAAAACACCCTTCCACGCCTT
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                                                                                                                                                  CAAAGTTTCAGAGGTCGGTCATATGCTCAAAGAAATGTACGAGCAATCGAGTAAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 1---ValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1214 CGAAGAATGGACCAAGTCATTGGCAGAAACAGAGACTAGAACAATCTGACATACCAAA
                                                                                                                                                                                            171 sProLeuAsp---***ThrGluGluLeuLeuLysTrp***AsnSerThr-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGAAAACCCATGATGCC---AATTTTTCTAACCGTCCGATTGATGGGGGCCCTACCTA
                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
                                                              CELLA, HARPER & SCINTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1927
141
101
212
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                          COMPUTER: IBM PS/V
COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AND Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/814,786
FILING DATE: 23-Mar-2001
PRIOR APPLICATION NUMBER: US/09/616,990
FILING DATE: 14-Jul-2000
APPLICATION NUMBER: US/09/616,990
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NOVEL PLANT GENES NUMBER OF SEQUENCES: 67 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: PETTY, LAWTENCE S.

REGISTRATION NUMBER: 31865
TELECOMUNICATION INFORMATION:
TELEFRA: 212-218-210
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1927 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 180 to 1748
IDENTIFICATION METHOD: by ex
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Campanula medium
                                                            ADDRESSEE: FITZPATRICK,
STREET: 30 Rockefeller |
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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575.50
48.02%
27.98%
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Query Match:
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ery Match: 23.98% Indels: 10 Gaps: 100 Gaps: 1	US-UG-80/-381-86 (1-341) X US-UG-814-786-1 (1-1824) Ov 1 MattentenGivten8latenGivten***Valten8latenbha***Histonbha		Qy 20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro*** 39	116 ATTCAACTCTTATTTCAAAACTACCGGCGGGATCTACCGGCCGGGGG 2	40 ProArgLanDroDhallaglvH;s**#H;sLanfveAsn[vs[anHallur]v	224 CCAAGAGGGTGGCCGGTGATCGGACCACTTCTAGGAGCCATGCCACATTT	Oy 59 Ala***IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMet 78	::: ::::::::::::::::::::::::::::::::::	Oy 79 ProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAla 98	Db 341 GGCATGGCAGTTGCTTCTACCCCTGATGCTGCTAAAGCATTCTTGAAAACACTTGAT 397	Qy 99 ThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*** 117	Db 398 AICAACTICICCAAIGGGCCACTAAIGCAGGIGCCACTCACTIAGCTFAAAGGTCAA 457	Qy 118 ***ValAla*****Pro**GlyProTyrTrp***PheValArqLysLeuIleMetAsn 137	Db 458 GACATGGTTTTGCACATTATGGACCACGATGGAAGTTGCTAAGGAAATTAAGCAACTTG 517	Qy 138 AspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArg 157	Db 518 CATATGCGCGAAAAGCCTTAGAGAATTGGGCAAATGGGCAATGAGCTAGGG 577	Oy 158 Lys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlu 177	Db 578 CACATGCTAAAATCAATGTCCGATATGAGTCGAGAGGGCCAGAGGGTTGTGGTGGCGGAG 637	Qy 178 GluLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193	DD 638 AIGTIGACATITGCCAIGGCCAATAIGAICGGACAAGGAGTGAIGCAAAGAGTATIT 697.	Oy 194GlualaGluGluIleArgAspIleAlaArgGluValLeuLysIle 208	698 GTAGATAAAGGTGTTGAGGTAAATGAATTTAAGGACATGGTTGTAGAGTTAATGACAATA 75	209 ***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLys	758 GCAGGGTATTTCAACATTGGTGATTTTATTCCTTGTTTAGCTTGGATGGA	Oy 229 TyrGluLySArgileAspAspIleLeuAsnLySPheAspFroValValGluArgValIle 248	מיני מיני מיני מיני מיני מיני מיני מיני	7	GATGAACACAAAGCAACTACCTATGAACGTAAGGGGAAACCAGATTTTCTTGATGTTGTT	Qy 259**AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeu 277	Db 938 ATGGAAAATGGGGACAATTCTGAAGGAGAA967	Qy 278 GluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeu 297	Db 968968968	Qy 298 ValValAsp***PheserAlaGly***AspSerThrAla*****ThrGluTrpAlaLeu 317	Db 998 TIGCIGAATITGICACAGCIGGIACGGACACIICITCIAGIGCAATAGAAIGGGCACII 1057
<pre>Qy 470 eAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSe 490</pre>	Qy 490 rMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLe 510	1658 TATGGAAGAGACTTTGGGATCGCATTGCAAAAAAAAAAA	old ualaargile	Db 1703 TECTGCTATT 1712	RESULT 5 US-09-814-786-1	; Sequence 1, Application US/09814786 ; Patent No. US2002100072A1	GENERAL INFORMATION: APPLICANT: KIKUMI, Yasuhiro	KIYOKAWA, Shigeto SHIRADA, Yukihisa		CKINAKA, Yasushi TITLE OF INVENTION: NOVEL PLANT GENES NIMARP OF SPOTTEMES 67	OF SECTION OF STATES OF ST	STREET: 30 Rockefeller Plaza	STATE: New York	COUNTRY: U.S.A. ; COUNTRY: 10112-3801	MEDIUM TYPES Diskette - 3.50 inch, 720 Kb storage.	CORFOLEN IN FO. W. S. SOFTWARE: PATENT AID Verl. 0	CURRENT APPLICATION DATA:		FILING DATE: 14-Jul-2000	: APPLICATION NUMBER: JP44963/92 FILING DATE: 02-MAR-1992	ATTORNEY/AGENT INFORMATION:  NAME: Perry, Lawrence S.	REGISTRATION NUMBER: 31865 TELECOMMUNICATION INFORMATION:	TELEPHONE: 212-2100 TELEFAX: 212-218-2200	RISTIC	LENGTH: 1824 Dase Pairs TYPE: nucleic acid	TOPOLOGY: linear MOISOTTE mybg: Dank	SOURCE	25 25	FEATURE: NAME/KEY: CDS	5 1633 STHOD: by	; SEQUENCE DESCRIPTION: SEQ ID NO: 1 US-09-814-786-1	Alignment Scores:	Fred. No.: 3.51e-74 Length: 1824 Score: 574.50 Matches: 151	Conservative: Mismatches:

DB: US-09-857-581-66 (1-521) x US-09-938-842A-1997 (1-1575)	26 SerLysAlaLeuArgHisLeuProAsnProProSerPro	Qy 46 GlyHis***HisLeuLesAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65	Qy 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaserThr 85	Qy 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105	Qy 106 GlnThrSerala***Arg***LeuThrTyrAsp*****Valala******Pro*** 124 :::	Oy 125 GlyProTyrTrp**PheValArgLySLeulleMetAsnAspLeuLeuAsnAlaThrThr 144	<pre>Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***NetAla 164</pre>	Qy 165 Gln***AlacluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp*** 183 :::	Qy 184 ASGETThr***SerWetMet	Oy 193 GlyGlualaGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyr 212	Qy 213 SerLeuThrAspPheile***ProLeuLys***LeuLysValGlyLysTyrGluLysArg 232 ::: ::	Qy 233 IleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg 252 :: ::	Qy 253 ***IleValArgArgArg***AsnGlyGlu******GluGlyGlu***SerGlyVal*** 272	Qy 273 LeuAspThrLeuLeuGluPheAlaGluAspGluThr**GluIleLysIleThrLys*** 292	Qy 293 ***IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla***** 312 :::	Qy 313 ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGlu 332	991 IOCGGATIOCOCCAIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProVal
Oy 318 AlaGluLeuIleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerVal 337		OY 358 IleValLysGluThrPheArgMetHisProProLeuProValValLysArgLysCys 376	Oy 377 ***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsn 396	QY 397 ValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGlu 416 ::	Oy 417 ArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***His 436	Oy 437 PheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThr 456	OY 457 SerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGly 476 :::    ::     :::     :::	Qy 477 ProGlnGlyGlnIleLeuLysGly***AspalaLysValSerMetGluGluArgAlaGly 496	Oy 497 LeuThrValProArgAlaHisSerLeuValCysValProLeu 510       :: ::      Db 1562 TTAGCTTTGCAGAAAGCTGTCCCTCTT 1588	RESULT 6 US-09-938-842A-1997 Sequence 1997, Application US/09938842A	GENERAL INFORMATION: APPLICANT: Harper, Jeff APPLICANT: Rreps, Joel	APPLICANT: WALLY AND APPLICANT: Zhu, Tong TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE	CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 FRIOR APPLICATION NUMBER: US 60/227,866	FRION ELLING DATE: 2000-08-24  PRIOR APPLICATION NUMBER: US 60/264,647  PRIOR FILING DATE: 2001-01-16  PRIOR APPLICATION NUMBER: US 60/300,111	FALOR LILING DAILS: ZUGI DO-12   NUMBER OF SEQ ID NOS: 5379   SEQ ID NO 1997   LENGTH: 1575   WINDER OF SEQ DAILS DAIL	; irrs: DNA ; ORGANISM: Arabidopsis thaliana US-09-938-842A-1997	lignment Scores: 3.32e-74 Length: core: 574.00 Matches: ercent Similarity: 47.41% Conservative:	29.68% Mismatches: 23.96% Indels:

46 GlyHis***HisLeuLeuLy	111:::111 212 GGTAGCATGATGGACCAAATAACTCACGTGGGTTAGCTAAACTAAG 2 66 LvsHisGlyProLeuPheSer*****PheGlySerMhrValValAlaSerThr 8	269 CAATATGGTGGGCTCTTTCATATGCGCATGGGGTACTTGCATATGGTCACTTTCATCTT 3  86 Progluteuphelvsteupheleugla************************************	329 CCTGAAATAGCTCGCCAAGTTCTGCAGGACAACATTTCTCCAACAGACCA	386 GCCAACATAGCCATAAGTTACTATAGTGATGGTGCAGAATAGCCTTTGCCCACTAC 44	125 GlyProTyrTrp***PheValargLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144	145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164	165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp 182	183 ***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200 511 ACCATGAACATCACTTACAGAGCTTTCGGGGCTAAAAATGAAGGACAGGATGAGTTC 670	201IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle	671	731 CCCTGGCTGGGTTGACCCCCAAGGGCTAGGGTTAGACTTGTCAAGGCTCGCAAG	239 LyspheaspprovalvalGluargValileLysLysargArg***IleValArgArgArg 258   1	259 ***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGlu 278	279 Phe	289 IleThrLys*****IleLysGlyLeuValValAsp***PheSeralaGly***AspSer 308	309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328	329 ***AlaArgGluGlu***TyrSerValValGlyLySASp**LeuValAspGluValAsp 348	349 ThrGinAsnLeuProTyrIleArgAlalleValLysGluThrPheArgMetHisProPro 368	369 LeuprovalValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro :::   :::::::::::::::::::::::::::::::
δò	qa ^o	I 8 8	7 6 6	ž d	d d	vy dq	QY Db	yo da	QY	<b>a</b> a ?	qa	QQ .	Qy Db	yo 'd	Oy Db	Q Q	Qy Db	۲۵ مرد د	Oy Coy
Db 1111 CCTTACCTACAAGGGTTATGAAAGAGACTCTTAGGCTTCACCCTACGCTTCTTT 1170	Qy .372 ValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAla 391	Leu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSer 4 AAGATTTTCATCAACGTTGGGGGATTCATAGAAATTGGGATGAACAAAC 1	412 Glu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla******LeuAsp	432 LeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg**MetCysProGly	Db 1330 TTCAATGGAGGTGATTTTAAGTACTTGCCTTTTGGGTCAGGAAGGA	Db 1390 ATTAACATGGTGAGAGTTGTTCTGTTCAACATGCTTCATTCA	Db 1450 TGGAAAGCACCTCAAGACAG	Db 1483 GAAGAGAAGTTTGGTCTTGTTCTTAAGTTGAAGTCTCCACTTGTGGCTATTCCTGTTCCA 1542  Qy 512 Argile 513	Db 1543 AGGTG 1548	RESULT 7 18-09-947-027-3 ; Sequence 3, Application US/09947027	Fatent No. US20020124281A1 GENERAL INFORMATION:	APPLICANT: Li, Laigeng TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIO TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS FITE PREFERENCE: 06600-0718	CURRENT APPLICATION NUMBER: US/09/947,027 CURRENT FILING DATE: 2001-09-05 PRIOR APPLICATION NUMBER: 60/230,086	NUMBER OF SECTION 14 TO 14 TO 15 TO	TYPE: DNA ORGANISM: aspen populus tremuloides FEATURE:		Anighment Scores: 2.57e-73 Length: 1764  Score: 568.50 Matches: 146  Percent Similarity: 46.14 Conservative: 87  Rest Total Similarity: 28.018 Misservative: 27	Match: 23.73% Indels: 4	US-09-857-581-66 (1-521) x US-09-947-027-3 (1-1764)  Qy 26 SerLysalaLeuargHisLeuProAsnProProSerPro***ProArgLeuProPheile 45

66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValalaSerThr 85 :::::	125 GlyProTyrTrp***PheValArgLySLeulleMetAsnAspLeuLeuAsnAlaThrThr	165 Gln***AlaGluala***LysProLeuAsp***ThrGluGluLeuLeuLysTrp 1	611 ACCATGACATCACTTACAGAGCAGCTTTCGGGGCTAAAAATGAAGGACAGGATCAGTTC 201IlealaargGluValLeuLySILe***GlyGluTyrSerLeuThrAspPheIle	0/1 219 731	239 LysPheAspProValValGluArgValIleLysLysArgArg**IleValArgArg 258	259 ***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGlu 	27.2 89.9 9.09	289 IleThrLys****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSer 308 :::	309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328	329 ***AlaArgGluGlu***TyrSerValValGlyLySA8p***LeuValAspGluValAsp 348	349 ThrGlnAsnLeuProTyrIleArgAlalleValLysGluThrPheArgMetHisProPro 368	369 LeuProValValLysArgLysCys***CluGluCys***IleAsnGly***Val***Pro 388	389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408 :::
	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2		an ko	da .	QQ DD	QQ ab	Q <i>y</i>	da da	40 60	Q0 Dp	Q.Y	40 Db
TrpAsp 408    -  -  -  -  -  -  -  -  -  -  -  -	CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerleulleGln 468           :::    TGCCCCGGTATGCAGCTTGGGTTATACACACTTGATTTGGCTGTTGCTCACTTGCTTCAT 148 CysPheAspLeuGlnValLeuGlyPrcGlnGlyGlnIleLeuLysGly***AspAlaLys 488	ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508 :::	1583 CCGAGCAAGCGTGTG 1597 SULT 8 -10-091-009-3 Sequence 3, Application US/10091009	OCCUPATION: Chiang, Vincent Lee C. Li, Laigeng INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND	NEWRITON: COMPOSITION, AND NEWRITON: CELLULOSE CONTENT IN PLANTS CENCE: 066040-9718 LILORIDON NUMBER: US/10/091, 009 LILOR DATE: 2007-03-06	PRIOR APPLICATION NUMBER: 09/947,027 PRIOR FILING DATE: 2001-09-05 PRIOR APPLICATION NUMBER: 60/230,086 PRIOR FILING DATE: 2000-09-05	NUMBER OF SEQ 1D NOS: 14 SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 1764	TYPE: DNA ORGANISM: aspen populus tremuloides FEATURE: NAME/KRY: misc feature	THER INFORMATION: CAldSH -091-009-3	Actidyment SCOIES: 2.57e-73 Length: 1764 Score: 568.50 Matches: 146 Percent Similarity: 46.14% Conservative: 87 Best Local Similarity: 28.91% Mismatches: 231	12.73% Indels: 12.73% Gaps: 12.73% Caps: 12.	26.1-06 (I 321) X US-10-U9I-UU9-3 (I-1/64) 26 SerbysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeuProPheIle 45 11	la***IleAspLeuSerLys 

us-09-857-581-66.p2n.rnpb

QY	409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428	Oy	63 LeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 82
Db	1319 GATCCTGATGCTTTTAAGCCTTCAAGGTTTTTGAAACCAGGGGTGCCT 1366	qa	199 TTAGCTAAAAAGTATGGCGGATTGTGCCCATCTCCGCATGGGATTCCTCCATATGTACGCT 258
QY	429 ***LeuaspLeuargGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448	δ, qa	83 AlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe*** 102
0y 17b	449 CysproGlyval***LeualaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468	Qy	103 ThrargPheGlnThrSerala***Arg***LeuThrTyrAsp*****Valala*** 121 
a do a	CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys	3	***Pro***GlyProTyrTrp***PheValArgLySLeuIleMetAsnAspLeuLeuAsn 14       :::    :::     :::
<b>q</b>	1481 TGTTTTACATGGGGAGTTGCCTGATGGCATGAAACCGAGTGAA 1522 489 Valsermerglugluardalaglyteumhrvalproardalattssertenvalcvsval 508	a è	
7 qa	CTTGACATGACTGATATGTTTGGACTCACCGCCAAGAGCAACTCGACTTGCTTTGCTTTTTTTT	r P	CCTAAAAGAGCTGAGTCATGGGCTTCAGTTCGTGATGAAGAGCACAAAATGGTCGG
Oy Db	509 ProLeuAlaArgile 513 	Qy	162 ***MetalaGln***AlaGluAla***LySProLeuAsp***ThrGluGluLeuLeuLys 181
RESULT US-09-	RESULT 9 US-09-938-842A-1506 . Common 1506 Partice HEVIOLOGOSOSACE	δλ S	182 Trp***AsnSerThr***SerMetMet***LeuGlyGluAlaGlu 196 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
GENE	nt No. US20020160378A1 RAL INFORMATION:	0 y	GlulleArgAsplleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAsp
APP APP TIT	A PELICANT: Wang, Xun APPLICANT: Wang, Xun APPLICANT: Zhu, Tong TITLE OF INVENTION: STRES-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE	3	Phelle***Proleulys***LeulysValGlyLysTyrGlulysArglleAsphaspile   -  -
; FIL ; CUR ; CUR ; PRI	E REFERENCE: SCRIP1300-3 THEN APPLICATION WOMBER: US/09/938,842A RENT FILING DATE: 2001-08-24 OR APPLICATION NUMBER: US 60/227,866	, va .	237 LeudanLysPheAspProValValGludrgValIleLysLysArgArg***IleValArg 256
PRI PRI PRI	OR FILING DATE: 2000-08-24  OR APPLICATION NUMBER: US 60/264,647  OR FILING DATE: 2001-01-16  OR APPLICATION NUMBER: US 60/300,111	O A	257 Argarg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThr 275 :::     781 AAGGAGAATCAAAACGCTGGGATGATGGGGATGTTGTGGATATGGATATGGTTGATGA
PRI NUM SEO	RIOR FILING DATE: 2001-06-22 UMBER OF SEQ ID NOS: 5379 Q ID NO 1506 LENGTH: 1563	O.y Db	276 LeuleuGlupheAlaGluAspGluThr
; TY ; OR US-09-	TYPE: DNA ORGANISM: Arabidopsis thaliana -09-938-842A-1506	QY	286 GlutleLystleThrLys********IleLysGlyLeuValValAsp***PheSeralaGly 305
Alignment Pred. No.: Score: Percent Si	Scores: 1.17e-72 563.50 milarity: 45.45%	Qy	306 ***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro*** 325 ::::::
Best L Query DB:	cal Similarity: 27.65% Mismatches: atch: 23.52% Indels: 9 Gaps:	QY	326 Valleu*****AlaargGluGlu***TyrSerValValGlyLysAsp***LeuValAsp 345
US-09-8 QY	57-581-66 (1-521) x US-09-938-842A-1506 (1-1563) 3 LeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro	, dg	346 GluValaspThrGlnAsnLeuProTyrIleArgalaIleValLysGluThrPheArgMet 365
DP QY	CTTGTCATCGTTGTCTCTTTTCATCTTCATCAGCTTCATCACACGGCGGGAAGGCCT ***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeu	Qy Dp	366 HisproproLeuProValValLysArgLysCys***GluGluCys***IleAsnGly*** 385
qq	115GGTTGG 141	0	386 Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVaiGly***Asp***Lys 405
Qy Db	43 ProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAsp 62	QO .	TTCATTCCCAAGAAATCTCGTGTGATGATCAACGCGTTTGCCATAGGACGCGACCCAACC
		QY	406 TyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGly 425

ValArgLysLeurleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgPro	LeudsollyspheaspprovalvalGluargvallleLysLysArgarg***IleValArg 25  [1]	valvaldy Lysasp***LeuvalaspoluvalaspThrGlnasnLeuProTyrIlearg 356  i::   :::   ::::   ::::     ::::
Db 1261 TCTTGGACTGGACACGTTTAGACATCGAGATTTTGGAACCGGGCGTACCG 1317  426 Gluala*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGly 445  1318GATTTCAAAGGGACAATTTGGACTTTATACCGTTCGGGTGGT 1362  446 Arg***MetCySProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSer 465  11363 CGTAGATCGTGCCCGGGTATGCAATTAGCGTTGACTTAGCCGTGGCTCAT 1422  456 LeuIleGlnCySPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLySGly***  466 LeuIleGlnCySPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLySGly***  466 LeuIleGlnCySPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLySGly***  476 LeuIleGlnCySPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLySGly***  477 AATTACATTGCTTCACGTGGAATTACCTGATGGGATG	RESULT 10 US-10-142-231-55 Sequence 55, Application US/10142231 Publication No. US20030077796a1 GENERAL INFORMATION: COTCHEAU. TILLE OF INVENTION: CATCHROME P450 OXYGENASES AND THEIR USES FILE REFERENCE: 62773 CURRENT FILING DATE: 2002-05-08 PRIOR RIPTOR TILING DATE: 1999-11-12 NUMBER OF SEQ ID NOS: 95 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 55 LENGTH: 1545 LENGTH: 1545 TYPE: DNA ORGANISM: Taxus cuspidata	Alignment Scores:    1.36e-72   Matches:   1545

:::   :::     ::::: :::	TTGATTTTGGGAAACGGCATTTTAACATCAATGATG euGlyGluala	AspilealaargGluValLeuLysile***GluTyrSerLeuThrAspPheile***    :::     ::::::	220 ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLys 239	240 PheaspProvalValGluArgValIleLysLysArgArg***IleVal 255	256 ArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThr 275 :::	276 LeuleuGluPheAlaGluAspGluThr***GluIleLysIleThrLys******IleLys 295	296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315	316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335 :::	336 ServalValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355	356 ArgalaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375	376 Cys**GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu***** 394	395 PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***Arg 414 11:::    :::     :::     ::: 1360 TTAAACATTTGGTGTATTCAGAGGGATCCACAGCTTTGGGAAAATCCTTTAGAATTCAAG 1419	415 ProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly 434	435 ***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCySProGlyVal***Leu 454 ::: :::	455 AlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 474 :::	475 LeuGlyProGlnGlyGlnIleLeuLySGly***AspAlaLysValSerMetGluGluArg 494 ::	495 AlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArg 512
DÞ OY	d o y	6 6 G	Q <i>y</i> Db	Qy	Qy Db	Oy Db	QY	. 0y	QY	до	da .	da Q	Qy Db	Oy Dp	QQ .	Qy Db	δλ
	Db 1474 GGACTCACAATGCCCAAAGCAGTTCCGTTGGAGACCATT 1512 RESULT 11 US-10-067-534-1	<pre></pre>	; APPLICANT: Tuo, Ping ; APPLICANT: Wang, Yan-Hong ; TITLE OF INVENTION: CDNA Clone of (+)-Delta-Cadinene-8-Hydroxylase Gene from Cotton ; FILE REFERENCE: 006602-113	CURRENT APPLICATION NUMBER: US/10/067,534 CURRENT FILING DATE: 2002-02-07 FRIOR APPLICATION NUMBER: US 60/267,160 FRIOR FILING DATE: 2001-02-07	; NUMBER OF SEQ 1D NOS: 19 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ 1D NO 1 ; LENGTH: 1933	; TYPE: UNA ; ORGANISM: Gossypium arboreum US-10-067-534-1	Alignment Scores: 1.92e-72 Length: 1933 Score: 563.00 Matches: 154 Percent Similarity: 45.72% Conservative: 92	23.50% Indels: 9 Gaps: (apr. 7.1021)	Oy 1 MetheuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeu 18  Oy 1 MetheuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeu 18  Oy 15.4 Angemententententententententententententente	19ArgProThPro***Ala***SerLysAlaLeuArgHisLeuPro 33	34 AsnProProSerPro***ProArgLeuProPhelleGlyHis***HisLeuLeuLys 11	53 AsplysleuLeuHisTyrAla***IleAspleuSerLysLysHysGlyProLeuPheSer	73 *****PheGlySerWetProThrValValalaSerThrProGluLeuPheLySLeuPhe 92	93 LeuGln******GlualaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 1::::::::::::::::::::::::::::::::::	113 LeuThrTyrAsp*****YalAla*****Pro***GlyProTyrTrp***Phe   :::   :::	131 ValargLysLeuIleMetasnAspLeuLeuAsnAlaThrThrValAsn***LeuArgPro	Db 544 AAGAGAAAAGIGCIGGTACGIGAAAIGCTIAGCCATAGIAGCATTAAAGCTTGTTATGGT 603 Oy 151 LeuargThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla*** 170

Db 1618 TITGGAATTAITAIGAAGAAAAGAAGCCITTAAITCTIGTICCIACACCAAGA 1671	Db 565 CAGAATTTCAATGAAAGCGGCTTTGTTATCGATCAAGACAGGATCGAAGAACTTGTT	AAGACAGGATCGAAGAACTTGTTACC 624
ULT 12 09-938-	Qy 204 GluvalleuLyslle***GlyGluTyrSerLeuTh  1	LeuThrAspPhelle***ProLeuLys*** 223
; Patent No. US20020160378A1 ; GENERAL INFORMATION:	224 LeuLysV	23
; APPLICANT: Harper, Jeff; APPLICANT: Kreps, Joel	9676 GG	7
APPLICANT: WANG, AND APPLICANT: Zhu, TRANSENCE Zhu, TRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE	Oy 237 LeuAsnLysPheAspProValValGluArgVallle	1e 248     TGATGATCACTTGAAGCCAGAGGGA 792
; FILE REFERENCE: SCRIP1300: : CURRENT APPLICATION NUMBER: US/09/938,842A; CURRENT FILING DATE: 2001-08-24	249	26
; PRIOR APPLICATION NUMBER: US 60/227,866 ; PRIOR FILING DATE: 2000-08-24	Db 793 AGAAAGAATCAAGATATTGTCACC	81
; PRIOR APPLICATION NUMBER: US 60/264,647 ; PRIOR FILING DATE: 2001-01-16 ; PRIOR APPLICATION NUMBER: US 60/300,111	Oy 269 SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLys :::        :: :: :::::::::::::::   Db 817TTGATTTTGGATATGATCGATAAACAAGAAGATTCAGATTCTTTCAAA	laGluAspGluThr***GluIleLys 288 :::::::::::::::::::::::::::::::::::
; PKIOK FILING DATE: 2001-06-22 ; NUMBER OF SEQ ID NOS: 5379 ; SEQ ID NO 2124 ; LENGTH: 1509	Qy 289 IleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSer :::	<pre>sp***Pheseralagly***Bspser 308                                       </pre>
; TYPE: DNA ; ORGANISM: Arabidopsis thaliana US-09-938-842A-2124	309	eulleAsnAsnPro***ValLeu*** 328
5.1e-72 Length: 559.00 Matches: 46.84% Conservati	0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
: 29.64% Mismatches: 23.33% Indels: 9 Gaps:	Qy 348 AspThrGlnAsnLeuProTyrIleArgAlaileValLysGluThrPheArgMetHisPro	alLysGluThrPheArgMetHisPro 367 ::
US-09-857-581-66 (1-521) x US-09-938-842A-2124 (1-1509)		
<pre>Qy 35 ProProSerPro**ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54                                     </pre>	o ro	17 6
* E * C * E	Qy 387 ***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyr	rpGlnValGly***Asp***LysTyr 406    :::
75 PheGlySerMetProThrvalValAlaSerThrProGluLeuPheLysLeuPheLeuGln 9	Qy 407 TrpaspargProserclu***ArgProGluargPheLeuGluThr***AlaGluGlyGlu 	heLeuGluThr***AlaGluGlyGlu 426 
<pre>zus cicdederciGifccGGfTGTGTGTGTCAACGGGAAGCAGCTGAAGCAGGTGCAAA z 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg**LeuThr 1 :::   </pre>	Oy 427 Ala****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg 	IntelleuProPheGlySerGlyArg 446 
268 ACCAATGACTIGGAAIGTIGCAGCCGAAGAAGACGGGGGAGGGGGAAAACTCTCT 115 TyrAsp****Valala****Pro***GlyProTyrIrp***PheValargLys	7 ***Me :: 4 AGGAT	<pre>1y***AlaThrLeuLeuAlaSerLeu 466 1</pre>
Db 325 TACGGTITCAAAGACAICACTITCGCACCAIACGGTGAGTAITGGCGAGAAGTGCGGAAAA 384 Qy 134 Leuilemetasnaspleuleuasnalaihithrvalasn***LeuargProLeuargthr 153     ::: :::   ::::   ::::	Qy 467 IleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIl :::	InGlyGlnIleLeuLysGly***Asp 486
Db 385 CTCGCGGTTATCGAQCTTTTAGCTCTAAAAAGGTTCAATCTTTCAGGTATATAAGAGAG 444  Qy 154 GlnGlnIleArgLys***Leuarg***MetalaGln***AlaGluala***LysProLeu 173	487	gAlaHisSerLeuval 50
445 GAAGAGTCGACTTCGTGGTCAAGAAAGTGTCAGAATCAGCTTTGAAGCAATCT	1432 507 CysVa	o # ⊣
Qy 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMet***LeuGly 193     :::::           505 GATTTAAGCAAAACCTTTTTCTCCCTCACCGCTAGTATCATTGTAGAGTCGCCTTAGGA 564	Db 1486 CTTGTGCCTGTTCAACGT 1503	
Qy 194 203   194 203   203	RESULT 13 US-09-878-574-72 ; Sequence 72, Application US/09878574	·

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193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrasp---*****Valala*****Pro***GlyProTyrTrp***PheValArgLys 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuleuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer*****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 GAAGAAGTTGCAGCCCTCGTTGATTTCATCAAACAAGCTGCTTCATTGGAGAAACCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                    ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ******GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu
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142
103
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                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                 PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 1491
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50.20%
29.10%
23.08%
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Best Local Similarity:
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Patent No. US20020160378a1
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US,09/9938,842A
CURRENT FILING DATE: Z001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 32-2115401)B
CURRENT APPLICATION NUMBER: US/09/876,574
FILE REFERENCE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
SEQ ID NOS: 15775
LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGACTCATCAACAATCCTAAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 ***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro*** 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValLeu******AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAsp 345
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                       TYPE: DNA OLYCINE MAX ORGANISM: Glycine max ORGANISM: Glycine Clone ID: LIB3028-056-Q1-B1-F1
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1191 AATCCAAACGTTTGGAAAGATCCAGAAGCTTTCATTCCCGAGAGGTTTATGGGATAGC--- 1247
                                                                                                                                                                                                                                                                                         ArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys***Ile 382
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                                                                                                                                            ***ValLeu*****AlaArgGluGlu***TyrSerValVal---GlyLysAsp***Leu 343
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   304
                         GGAATAGACACTTCTGCACAAGTTATGACATGGGTGATGACATATTTGATTTCAAACCCA
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---GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***PheSerAla
                                                                                                                                                                               954 AGAGTTTTGAAGAAAGCGCAGGCCGAGGTGAGAAGTGATAAAACACAAAGATGATATC
                                                                                                                                                                                                                  ValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPhe
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                                                                      Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro
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Publication No. US20030077796A1

GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
FILE REFERENCE: 62773
CURRENT PFLING DATE: 2002-05-08

PRIOR APPLICATION NUMBER: 60/165,250

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 53
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FEATURE:
NAME/KEY: misc_feature
COCATION: (1)..(1539)
US-10-142-231-53
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                                                                                                                                                                           06 CIGCGCGGGCTGAGAACAATGGAAGAATTGCCCCCCCGGCCCAATTCCA---TGGCCG
                                                                                                                                                                                                                                                                     SerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAla
                                                                                                                                                                                                                                                                                                                                                                                         ArgPheGlnThrSerAla***Arg***LeuThrTyrAsp---****ValAla*****
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAla
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            1539
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           Length:
Matches:
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Mismatches:
Indels:
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Best Local Similarity:
Query Match:
Alignment Scores:
Pred. No.:
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e e	494 ArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArg1le 513	λy 4
64	1438 ATTGAAGGAGAGTTGGATGAA 1464	)b 14
· •	474 ValLeuGlyProGlnGlyGlnIleLeuLySGly***AspAlaLySValSerMetGluGlu 493	2y 4
37	78 ATGCCCGTTGTGACGATGGAACATGCGTTGGCACAACTCATGCACTGCTTCCAGTGCGC 1437	)b 13
	454 LeualaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCySPheAspLeuGln 473	λy 4
77	18 AAAGAGITTTTCGATATGGTTCCCTTTGGTGCGGGAAGGAAGGATGCCCAGGGCCAAGC 13	jb 13
	434 Gly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCySProGlyVal*** 453	2y 4
17	73 AAACCAAAAAGATTTTTGGCCANAAATGTGGACTTGCAAAAGGA 1317	)b 12
e.	414 ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArg 433	λy 4
72	13 CICGITAACGCGIGGGCGAIAGGAAAAGAICCAAACGIGIGGGAIGAIGCCCIGGCAIIC 12	b 12
8	394 ***PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu*** 413	3
12	53 CACGAATCGACCCAAGATTGCACTGTCAATGGATACTTCATTCCTGAAAGAACCAGAATT 12	3b 11
m	374 ArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*** 393	λy 3
52	1093 CIGCAAIGTGGGGAAAAAGACGAIGAGATTATATCCGGCGGGGGGCCTTTGCTTATCCCG 1152	10 qc
æ	355 IleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLys 373	λy 3
92	1033 GAATCCGTTGTGGGAAGAAAGAGGGTGGTGAAAGAAATGATCTGGGAAAGTATGGAATAC 1092	op 10
4	335 TyrserValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyr 354	λy 3

Search completed: June 1, 2003, 03:04:32 Job time: 258 secs

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GENERAL INFORMATION:
APPLICANT: B. I. du Pont de Nemours and Company
ITILE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERRORS: BB1339 PCT
CURRENT APPLICATION UNDBER: US/09/887,581
CURRENT FILING DATE: 2001-06-05
                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                       February 26, 2004, 16:59:35; Search time 1 Seconds (without alignments) 5.031 Million cell updates/sec
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Sequence 34,
Sequence 36,
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1 MLLELALGLXVLALFXHLRP.....AHSLVCVPLARIGVASKLLS
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
                                                                                                                                    BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                   19 seqs, 9656 residues
                                                                                                                                                                                                          length: 0
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Maximum DB seq
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TITLE OF INVENITION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PLING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFFWARE: Microsoft Office 97
SEQ ID NO 26
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87.1%; Pred. No. 0;
tive 67; Mismatches
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFWMARE: Microsoft Office 97
LENGTH: 521
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Best Local Similarity
Matches 454; Conservat
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US-09-857-581-26
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| Sequence 30, Application US/09857581
| Sequence 30, Application US/09857581
| SEMERAL INFORMATION:
| APPLICANT: E 1. du Pont de Nemours and Company
| TITLE OF INFORMION Nucleic Acid Sequences Encoding Isoflavone Synthase
| TITLE DE INFORMION NUMBER: US/09/857,581
| CURRENT FILING DATE: 1201-06-05
| PRIOR APPLICATION NUMBER: 60/117,769
| PRIOR APPLICATION NUMBER: 60/117,769
| PRIOR FILING DATE: 1999-01-27
| PRIOR FILING DATE: 1999-03-24
| PRIOR FILING DATE: 1999-09-24
| NUMBER OF SEQ ID NOS: 66
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 30
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MILELALGLXVLALFXHLRPTPXAXSKALRHLPNPPSPXPRLPF1GHXHLLKDKLLHYAX
               1 MLDELALGILIVLALFLHIRPTPTAKSKALRHIPNPPSPKPRLPFIGHLHILKDKLHYAL
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67; Mismatches
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red. No. 0;
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Best Local Similarity 87.1%;
Matches 454; Conservative 67
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US-09-857-581-30
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US-09-857-581-30
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
TITLE REPERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: 05/09/857,581
CURRENT PILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 66
SOCIETY APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 28
LENGTH: 521
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67; Mismatches
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                                                                            Query Match
Best Local Similarity 87.1:
Matches 454; Conservative
                                   ; ORGANISM: Phaseolus aureus
US-09-857-581-26
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Best Local Simi
Matches 454;
           LENGTH: 521
TYPE: PRT
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Sequence 34, Application US/09857581

GENERAL INFORMATION:
APPLICANT'E E. I. dw Pont de Nemours and Company
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT APPLICATION NUMBER: 00/117,769
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 60/114,783
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: MICROSOft Office 97
SEQ ID NO 34
LENGTH: 5.1
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; Pred. No. 0;
67; Mismatches
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Best Local Similarity 87.1%;
Matches 454; Conservative 6
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) ORGANISM: Trifolium pratense
US-09-857-581-34
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GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours and Company

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

FILE REFERENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 2001-06-05

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR PLING DATE: 1999-02-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

SEQ ID NO 32

LENTH: 521
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100.0%; Score 2396;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches
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; ORGANISM: Trifolium pratense
US-09-857-581-32
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               1 MLIELALGLEVLALFLHLRPTPSAKSKALRHLPNPPSPKPRLPFIGHLHLLKDKLLHYAL 60
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100.0%; Score 2396;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches
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US-09-85-581-36
Sequence 36, Application US/09857581
GENERAL INFORMATION:
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ORGANISM: Pisum sativum
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US-09-857-581-36
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GENERAL INVERTION:

JAPLICANT: E. I. du Pont de Nemours and Company

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

FILE REFERENCE: Ball 339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR PLILING DATE: 1999-01-27

PRIOR PLILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-27

PRIOR PLILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

SPRIOR FILING DATE: 1999-07-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

LENGTH: 522
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GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPRENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
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67; Mismatches
Application US/09857581
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Best Local Similarity 87.1%; I
Matches 454; Conservative 67;
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     Sequence 24, Applica GENERAL INFORMATION:
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Sequence 20, Application US/09857581

Sequence 20, Application US/09857581

SEQUENCE INFORMATION:

APPLICANT E. I. du Pont de Nemours and Company

ITILE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;

ITILE REFERENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT PILING DATE: 1999-01-06-05

PRIOR PILING DATE: 1999-01-27

PRIOR PLILING DATE: 1999-07-20

PRIOR PLILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR PLILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/156,094

PRIOR FILING DATE: 1999-07-24

NUMBER OF SEQ ID NOS: 66

SOFUTHARE: Microsoft Office 97

SEQ ID NO 20

IENGTH: 499
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Best Local Similarity 86.8%; Pred. No. 0;
Matchés 433; Conservative 66; Mismatches
                                                                                                                                        96.2%; Score 2304; D
86.8%; Pred. No. 0;
ive 66; Mismatches
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Matches 433, Conservative
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ORGANISM: Lens culinaris
US-09-857-581-20
                                               TYPE: PRT
CRGANISM: Vicia villosa
US-09-857-581-18
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    SEQ ID NO 18
LENGTH: 499
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US-09-857-581-18
US-09-857-581-18
SQUENCE 18, Application US/09857581
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;
FILE REFERENCE: B81339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1999-01-66-05
PRIOR FILING DATE: 1999-01-27
PRIOR PLICATION NUMBER: 60/117,769
PRIOR PLICATION NUMBER: 60/144,783
PRIOR PLICATION NUMBER: 60/144,783
PRIOR PLICATION NUMBER: 60/144,783
PRIOR PLICATION NUMBER: 60/144,783
PRIOR PLICATION NUMBER: 60/156,094
PRIOR PLING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
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86.8%; Pred. No. 0;
ive 66; Mismatches
CURRENT FILING DATE: 2001-06-05
PRIOR PEDELACHION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR PILING DATE: 1999-09-24
NUMBER: OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
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Matches 433; Conservative
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CRGANISM: Medicago sativa
US-09-857-581-16
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| Sequence 40, Application US/09857581
| Sequence 40, Application US/09857581
| GENERAL INFORMATION:
| APPLICANT: E. I. du Font de Nemours and Company
| TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
| FILE REPRENCE: BB1339 PCT
| CURRENT APPLICATION NUMBER: US/09/857,581
| CURRENT PILING DATE: 1999-01-27
| PRIOR FILING DATE: 1999-01-27
| PRIOR FILING DATE: 1999-07-20
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96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels
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; LENGTH: 499
; TYPE: PRT
; ORGANISM: Trifolium repens
US-09-857-581-40
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US-09-857-581-40
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GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TILLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;
FILE REFERENCE: BB1339 FCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1099-01-27
PRIOR PELICATION NUMBER: 60/117,769
PRIOR PELICATION NUMBER: 60/117,769
PRIOR PELICATION NUMBER: 60/144,783
PRIOR PELICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 66
SOFTWARR: Macrosoft Office 97
SEQ ID NOS: 66
SEQ ID NOS: 66
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                        FXHLRPTPXAXSKALRHLPNPPSPXPRLPFIGHXHLLKDKLLHYAXIDLSKKHGPLFSXX
                                                                                                FGSMPTVVASTPELFKLFLQXXEATSFXTRFQTSAXRXLTYDXXVAXXPXGPYWXFVRKL
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Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0;
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Sequence 55, Application US/09857581
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-24
NUMBER OF SEQ ID NOS: 66
SEQ ID NOS: 66
SEQ ID NOS: 66
LEMOTH: 499
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                                     435 XHFQLLPFGSGRXMCPGVXLATSGXATLLASLIQCFDLQVLGPQGQILKGXDAKVSMEER
                                                             61 FGSMPTVVASTPELFKLFLQTHEATSFNTRFQTSAIRRLTYDSSVARVPFGPYWKFVRKL
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96.2%; Score 2304; D
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches
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US-09-857-581-55
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US-09-857-581-55
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US-09-857-581-48

SQUENCE 48 Application US/09857581

GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours and Company

TILE REFERENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR FILING DATE: 1999-07-20

SEQ ID NOS: 66

SOFTWARE: MICROSOFT Office 97

SEQ ID NO 48

LENTH: 499
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                                                                                301 WALAELINDPKVLQKAREEAYSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKR 360
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KCXEECXINGXVXPEGALXXFNVWQVGXDXKYWDRPSEXRPERFLETXAEGEAXXLDLRG 434
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86.8%; Pred. No. 0;
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Best Local Similarity 86.8
Matches 433; Conservative
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CORGANISM: Beta vulgaris
US-09-857-581-48
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Sequence 57, Application US/09857581

Sequence 57, Application US/09857581

GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours and Company

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

FILE REPRENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT APPLICATION NUMBER: 60/117,769

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 57

SEQ ID NO 57
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4.09-857-581-59
5.09-867-581-59
GENERAL INFORMATION:
7. APPLICANT: E. I. du Pont de Nemours and Company
7. TITLE OF INVENTIAN Nucleic Acid Sequences Encoding Isoflavone Synthase
7. FILE REPERENCE: 881339 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                            15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFIGHXHLLKDKLLHYAXIDLSKKHGPLFSXX
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86.8%; Pred. No. 0;
iive 66; Mismatches 0;
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Best Local Similarity 86.8
Matches 433; Conservative
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, ORGANISM: Medicago sativa
US-09-857-581-57
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Sequence 38, Application US/09857581
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT APPLICATION NUMBER: 60/117,769
FRIOR APPLICATION NUMBER: 60/117,769
FRIOR APPLICATION NUMBER: 60/117,769
FRIOR FILING DATE: 1999-01-27
FRIOR APPLICATION NUMBER: 60/144,783
FRIOR FILING DATE: 1999-07-20
FRIOR APPLICATION NUMBER: 60/156,094
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
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96.2%; Score 2304; D
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-09-04
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 66
SOSTWARE: MICROSOFT OFFICE OFFICE
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US-09-857-581-59
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US-09-857-581-38
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TYPE: PRT
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GENERAL INCURRATION:

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERENCE: Bala 39 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 2001-06-05

PRIOR RELING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-09-44

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

SEQ ID NO 61

LENGTH: 498
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Pred. No. 0;
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86.7%; Pred. No. 0;
iive 66; Mismatches 0;
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US-09-857-581-61
Sequence 61, Application US/09857581
GENERAL INFORMATION:
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SOFTWARE: Microsoft Office 97
SEQ ID NO 38
LENGTH: 498
                                           TYPE: PRT; ORGANISM: Trifolium repens
US-09-857-581-38
                                                                                                                              Conservative
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; ORGANISM: Beta vulgaris
US-09-857-581-61
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Best Local Similarity
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Best Local Similarity
Matches 432; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CXEECXINGXVXPEGALXXFNVWQVGXDXKYWDRPSEXRPERFLETXAEGEAXXLDLRGX 435
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                                                                      GSMPTVVASTPELFKLFLQXXEATSFXTRFQTSAXRXLTYDXXVAXXPXGPYWXFVRKLI
                                              16 XHLRPTPXAXSKALRHLPNPPSPXPRLPFIGHXHLLKDKLLHYAXIDLSKKHGPLFSXXF
1; Indels
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    431; Conservative
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completed: February 26, 2004, 16:59:38 e : 3 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

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5.031 Million cell updates/sec March 1, 2004, 07:06:46; Search time 1 Seconds

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Run

af135484pep 2679 1 MILELALGLIVLALFLHLRP.....AHSLVCVPLARIGVASKILS 521 Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

19 seqs, 9656 residues Searched:

Total number of hits satisfying chosen parameters:

13

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

ramirez581.pep:\* Database :

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appl	App1	Appl									
ď	26,	24,		30,	-	~		36,											38,
Description	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence		Seguence	Sequence	Seguence	Seguence	Seguence	Seguence
QI	JS-09-857-581-26	US-09-857-581-24	US-09-857-581-28	US-09-857-581-30	US-09-857-581-34	US-09-857-581-32	US-09-857-581-2	US-09-857-581-36	US-09-857-581-59	US-09-857-581-22	US-09-857-581-48	US-09-857-581-18	US-09-857-581-55	US-09-857-581-57	US-09-857-581-40	US-09-857-581-61	US-09-857-581-20	JS-09-857-581-16	US-09-857-581-38
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Score	99	2667	99	2665	99	9	61	S	2563	55	2553	54	2544	2539	52	2525	ဌ	2498	47
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## ALIGNMENTS

Sequence 24, Application US/09857581

Sequence 24, Application US/09857581

GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR PAPLICATION NUMBER: 60/147,783
PRIOR PRILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
SEQ ID NOS: 66
SEQ ID NO 24

US-09-857-581-24

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Sequence 26, Application US/0985781
GENERAL INFORMATION:
APPLICANT: E. 1. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERENCE: BB139 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
RESULT 1
US-09-857-581-26
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Pred. No. 0;
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR PRIOR PRING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFWMARE: Microsoft Office 97
LENGTH: 521
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Best Local Similarity 99.6%;
Matches 519; Conservative
                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Phaseolus aureus
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GENERAL INFORMATION:
APPLICANTE E. I. dw Pont de Nemours and Company
APPLICANTE. E. I. dw Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/095 S57, S81
CURRENT FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: MICROSOFT Office 97
LENGTH: 521
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Pred. No. 0;
0; Mismatches 2;
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Pred, No. 0;
0; Mismatches
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Conservative (
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      ; LENGTH: 522
TYPE: PAT
; ORGANISM: Phaseolus aureus
US-09-857-581-24
                                                                              Query Match
Best Local Similarity 99.6
Matches 519; Conservative
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Best Local Similarity
Matches 519; Conserv
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JENERAL INTOKATION:

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

FILE REFREENCE:

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR PRIOR DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR PILING DATE: 1999-00-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

SEQ ID NO 30

LENGTH: 521

TYPE: PRT

TYPE: PRT

GENERAL INTOKATOR AURGUS

US-09-857-581-30
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.6%;
Matches 519; Conservative
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: E. I. dw Pont de Namours and Company

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

FILE REFERENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

SEQ ID NO 32

LEMOTH: 521
                                                                                                                                                                                                                                                     61 IDLSKKHGPLFSLYFGSMPTVVASTPBLFKLFLQTHBATSFNTRFQTSAIRRLTYDSSVA 120
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Best Local Similarity 99.2%; Pred. No. 0;
Matches 517; Conservative 0; Mismatches
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; ORGANISM: Trifolium pratense
US-09-857-581-32
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US-09-857-581-32
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GENERAL INFORMATION:
APPLICANT: E. I. dw Font de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2011-06-05
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 34
LENTH: 521
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    DPVVERVIKKRREIVRRKKNGEVVEGEVSGVFLDTLLEFÄEDETMEIKITKDHÍKGLVVD 300
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99.6%; Pred. No. 0;
ive 0; Mismatches
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US-09-857-581-34
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Matches 519; Conservative
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US-09-857-581-34
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GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours and Company
ITILE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERBRE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PLING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-24
NUMBER OF SEQ ID NOS: 66
SOFTHARE: M:COGOÉT Office 97
SEQ ID NO 36
LENGTH: 521
              5-09-857-581-36
Sequence 36, Application US/09857581
GENERAL INFORMATION:
APPLICANT: B. I. du Pont de Nemours
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Best Local Similarity 96.4
Matches 502; Conservative
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ORGANISM: Pisum sativum
US-09-857-581-36
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| Sequence 2, Application US/09857581
| Sequence 2, Application US/09857581
| GENERAL INFORMATION:
| APPLICANY: E. I. du Pont de Nemours and Company
| TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
| FILE REPERENCE: BB1339 PC7.
| FILE REPERENCE: BB1339 PC7.
| CURRENT APPLICATION NUMBER: US/09/857,581
| CURRENT FILING DATE: 2001-06-05
| PRIOR APPLICATION NUMBER: 60/117,769
| PRIOR APPLICATION NUMBER: 60/144,783
| PRIOR APPLICATION NUMBER: 60/126,094
| PRIOR FILING DATE: 1999-09-24
| NUMBER OF SEQ ID NOS: 66.024
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                                                                                                               ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
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Pred. No. 0;
8; Mismatches
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SEQ ID NO 2
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Glycine max US-09-857-581-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 507; Conserv
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Best Local
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ITILE OF INVENTION: Uncleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
                                                                                                1 MELELALGELVLALFEHERPTPTAKSKALRHEPNPPSPKPREPFIGHLHELKDKELHYAL
                                                                                                                                                                                                                                                                                                     121 MVPFGPYWKFVRKLIMNDLLNATTVNKLRPLRTQQIRKFLRVMAQGABAQKPLDLTEBLL
                                                                                                                                                                                                                                                                                                                                  421 TGAEGEAGPLDLRGQHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGQ
DB 1; Length 521;
                                                Indels
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                                                12; Mismatches
96.9%; Score 2596; 96.4%; Pred. No. 0;
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APPLICANT: B. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE RERERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-24
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 48
LENGTH: 499
                                                                                                                                                                                                                                                                                                                                                             61 FGSMPTVVASTPELFKLFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPYWKFVRKL 120
                                                                                                                                                                                                                                                                                                                                                                                                             IMNDLLNATTVNKLRPLRTQQIRKFLRVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGE 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 ABBIRDIAREVLKIFGEYSLTDFIWPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AESIRDIAREVLKIFGEYSLTDFIWPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREI
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95.3%; Score 2553; C
Best Local Similarity 99.2%; Pred. No. 0;
Matches 495; Conservative 0; Mismatches
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                                                                                                                                     95.3%; Score 2554;
99.0%; Pred. No. 0;
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US-09-857-581-48
Sequence 48, Application US/09857581
GENERAL INFORMATION:
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                                                                                                                                       Query Match
Best Local Similarity 99.0
Matches 494; Conservative
; SEQ ID NO 22; LENGTH: 499; TYPE: PRT TO OCANISM: Lens culinaris US-03-857-881-22
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US-09-857-581-48
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GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT APPLICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
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  CURRENT FILING DATE: 2001-06-05
PRIOR PEPLOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR PELING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
NUMBER: OF SEQ ID NOS: 66
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 59
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                                                                                                                                                                                                                                                                               ; ORGANISM: Medicago sativa
US-09-857-581-59
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Best Local Similarity
Matches 495; Conserva
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US-09-857-581-22
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Gaps

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Sequence 55, Application US/09857581
GENERAL INFORMATION:
APPLICANT E I. dw bont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: 08/09/857,581
CURRENT APPLICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 55
LENGTH: 499
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Pred. No. 0;
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Best Local Similarity 98.8%;
Matches 493; Conservative
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US-09-857-581-55
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

rich Reference: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR APPLICATION NUMBER: 60/114,783

PRIOR PILLING DATE: 1999-01-27

PRIOR PILLING DATE: 1999-07-20

PRIOR PILLING DATE: 1999-07-20

PRIOR PILLING DATE: 1999-07-20

SPRIOR PILLING DATE: 1999-07-20

SPRIOR FILLING DATE: 1999-07-20

SPRIOR FILLING DATE: 1999-07-20

SPRIOR FILLING DATE: 1999-08-44

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

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Best Local Similarity 98.8%;
Matches 493; Conservative
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US-09-857-581-18
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GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERBNCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-027
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-07-20
SPRIOR PELING DATE: 1999-07-20
SPRIOR PELING DATE: 1999-07-20
SPRIOR APPLICATION UMBER: 60/156,094
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 40
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361 KCTEECEINGYVIPEGALILFNVWQVGRDSKYWDRPSEFRPERFLETGAEGEARPLDLRG 420
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Best Local Similarity 97.6%; Pred. No. 0;
Matches 487; Conservative 6; Mismatches
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US-09-857-581-40
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US-09-857-581-40
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PELICATION NUMBER: 60/144,783
PRIOR PELICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 57
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                      VRRRKNGEVVEGEVSGVLLDTILLEFAEDETMEIKITKDHIKGLVVDFFSAGTDSTAVATE 300
                                                                     374
                                                                                                                                                              KCTEECEINGYVIPEGALILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRG 434
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 98.8%;
Matches 493; Conservative
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US-09-857-581-57
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CURRENT APPLICATION NUMBER: US/09/857,581
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                                                                   Sequence 61, Application US/09857581

Sequence 61, Application US/09857581

GENERAL INFORMATION:
APPLICANT's E. I. dw Pont de Nemours and Company
ITILE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT PILING DATE: 1099-01-06-05

PRIOR PILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/114,769

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-27

PRIOR PELING DATE: 1999-02-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

SEQ ID NO 61
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98.2%; Pred. No. 0;
:ive 2; Mismatches
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Best Local Similarity 98.2
Matches 489; Conservative
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, ORGANISM: Beta vulgaris
US-09-857-581-61
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APPLICANT: E. I. du Pont de Nemours and Company TITLE OF INNENTION: Norleic Acid Sequences Encoding Isoflavone Synthase FILE REFERENCE: BB1339 PCT

US-09-857-581-20; Sequence 20, Application US/09857581; GENERAL INFORMATION:

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Sequence 16, Application US/09857881

GENERAL INFORMATION:
APPLICAMY:
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;
TITLE OF INVENTION: Number: US/09/857,581
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR PILING DATE: 1999-07-20
PRIOR APPLICATION UNDER: 60/156,094
NUMBER OF SEQ ID NOS: 66
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; Pred. No. 0;
7; Mismatches
CURRENT FILING DATE: 2001-06-05
PRIOR PEDELORION NUMBER: 60/117,769
PRIOR PELING DATE: 1999-01-27
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER: OF SEQ ID NOS: 66
SOFTWARE: MICROSOFT Office 97
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 AGLTVPRAHSLVCVPLARI 513
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.4%;
Matches 486; Conservative
                                                                                                                                                                                                                                                                                 LENGTH: 499
TYPE: PRT
CORGANISM: Lens culinaris
US-09-857-581-20
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US-09-857-581-16
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Gaps ö

10; Indels

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SMPTVVASTPELFKLFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPYWKFVRKLIM 136
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                                                                                                                                                                                                                                                                                                          122 NDLENATTVNKLRPERTQQIRKFERVMAQSAEAQKPEDVTEELLKWTNSTISMMIGEAE 181
                                                                                                                                                                                                                                                                                                                                                                 BIRDIAREVLKIFGEYSLTDFIWPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVR 256
                                                                                                                                                                                                                                                                                                                                                                                            182 BIRDIAREVLKIFGEYSLIDFIWPLKYLKVGKYEKRIDDILNKFDPVVERVIKKRREIVR 241
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                                                                                    2 HIRPTESAISKALRHIPNPPSPRPRLPFIGHLHILKDKLLHYAPIDLSKKHGPLFSLSFG
                                                      HLRPTPTAKSKALRHLPNPPSPKPRLPFIGHLHLLKDKLLHYALIDLSKKHGPLFSLYFG
     477; Conservative 10; Mismatches
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ne : 2 secs
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| GENERAL INFORMATION: | APPLICANT: = 1. du Pont de Nemours and Company |
| TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase |
| FILE REFERENCE: BB1339 PCT |
| CURRENT APPLICATION NUMBER: US/09/857,581 |
| CURRENT FILING DATE: 2001-06-05 |
| PRIOR PILING DATE: 1999-01-27 |
| PRIOR PILING DATE: 1999-07-20 |
| PRIOR PILING DATE: 1999-07-20 |
| PRIOR PILING DATE: 1999-07-20 |
| PRIOR FILING DATE: 1999-07-20 |
| PRIOR FILING DATE: 1999-07-20 |
| SEQ ID NOS: 66 |
| SOFTWARE: Microsoft Office 97 |
| LENTH: 498 |
| LENTH: 498 |
| CONTINUED OF SEQ ID NOS: 66 |
| LENTH: 498 |
| CONTINUED OF SEQ ID NOS: 66 |
| LENTH: 498 |
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| CONTINUE
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Pred. No. 0;
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; ORGANISM: Trifolium repens
US-09-857-581-38
SOFTWARE: Microsoft Office
SEQ ID NO 16
LENGTH: 499
                                                                       TYPE: PRT; ORGANISM: Medicago sativa
US-09-857-581-16
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Best Local Similarity
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US-09-857-581-38
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Best Local S
Matches 481
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model March OM protein Run on:

1, 2004, 07:04:37 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

af022462pep

2683 1 MILELALGILVIALFIHIRP.....AHSIVCVPIARIGVASKILS 521 Perfect score: Sequence:

**BLOSUM62** Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 19 seqs, 9656 residues

19

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

ramirez581.pep:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 26, Appl	24,	N	m	m	Sequence 32, Appl	7	36,	Ŋ	22,	48,	18,	Sequence 55, Appl	57,	Sequence 40, Appl	Sequence 61, Appl		Sequence 16, Appl	Sequence 38, Appl	
QI	US-09-857-581-26	US-09-857-581-24	US-09-857-581-28	US-09-857-581-30	US-09-857-581-34	US-09-857-581-32	US-09-857-581-2	US-09-857-581-36	US-09-857-581-59	9-857-581-2	US-09-857-581-48	US-09-857-581-18	US-09-857-581-55	US-09-857-581-57	US-09-857-581-40	US-09-857-581-61	US-09-857-581-20	US-09-857-581-16	US-09-857-581-38	
n DB	7	7	1	7	1	1 1	1 1			Б		9	6		7			9	н 8	
Length	521	N	N	52	N	52	N	N	49	σ	a)	49	49	49	49	49	49	49	49	
% Query Match	98.86	98.8	98.7	98.7	98.7	98.2	96.8	96.2	94.9	94.6	94.6	94.4	94.2	94.0	93.6	93.5	93.3	92.5	91.6	
Score	9	2651	64	2649	64	m	59	2580	2547	53	2537	2532	52	2523	51	50	50	2482	45	
Result No.	1	7	m	4	ß	ø	7	œ	σι	10	11	12	13	14	15	16	17	18	19	

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Sequence 26, Application US/09857581
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TILES OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
US-09-857-581-26
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61 IDLSKKHGFLFSLXFGSMPTVVASTPELFKLFLQTHEATSFNTREQTSAIRRLTYDSSVA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 FFSAGTDSTAVATEWALAELINNPKVLEKAREEVYSVVGKDRLVDEVDTQNLPYIRAIVK 360
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR PAPLICATION NUMBER: 60/117,769
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR PLING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR PLING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
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Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 26
LENGTH: 521
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CRGANISM: Phaseolus aureus
US-09-857-581-26
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Best Local Similarity 99.0%;
Matches 516; Conservative
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ORGANISM: Phaseolus aureus
US-09-857-581-30
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Sequence 28, Application US/09857581
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SEQUENCE 28, Application US/09857581
STITE OF INTERNATION:
TITLE OF INTERNATION NUMBER: US/09/857,581
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR APPLICATION NUMBER: 60/114,783
PRIOR APPLICATION NUMBER: 60/114,783
PRIOR PLILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-09-4
NUMBER OF SEQ ID NOS: 66
SOPTWARE: Microsoft Office 97
LINGTH: 521
LINGTH: 521
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Pred. No. 0;
1; Mismatches 4;
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                                                                     Score 2651;
Pred. No. 0;
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Best Local Similarity 99.0%;
Matches 516; Conservative
                                                                     98.8%;
                 TYPE: PRT
CRGANISM: Phaseolus aureus
US-09-857-581-24
                                                                     Query Match
Best Local Similarity 99.0
Matches 516; Conservative
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERRINCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1099-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-01-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 30
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1 MILELALGILVIALFIHLRPTPTAKSKALRHIPNPPSPKPRLPFIGHLHILKDKLHYAL
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APPLICANT: B. 1. du Pont de Nemours and Company
JAPLICANT: B. 1. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 FCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 32
LENGTH: 521
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  DPVVERVIKKRREIVRRRMGEVVBGEVSGVFLDTLLEFAEDETTEIKITKDHIKGLVVD 300
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Pred. No. 0;
1; Mismatches
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Best Local Similarity 98.7%;
Matches 514; Conservative
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CRGANISM: Trifolium pratense
US-09-857-581-32
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CURRENT FILING DATE: 2001-06-05

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-07-20

PRIOR PELING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/156,094

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

LENGTH: 521
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llarity 99.0%;
Conservative
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US-09-857-581-34
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Matches 516; Conserv
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US-09-857-581-34
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; Sequence 59, Application US/09857581; GENERAL INFORMATION:
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Matches 499; Conserv
RESULT 8
US-09-857-581-36
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LENGTH: 521
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                           TGAEGEARPLDIRGOHFOLLPFGSGRRMCPGVNLATSGMATLLASLIOCFDLOVLGPOGO 480
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TILE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-66-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PLING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR RILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
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Pred. No. 0;
                                                                                                                                                 US-09-857-581-2; Sequence 2, Application US/09857581; GENERAL INFORMATION:
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Best Local Similarity 96.7%;
Matches 504; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
; ORGANISM: Glycine max
US-09-857-581-2
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Sequence 36, Application US/09857581

Sequence 36, Application US/09857581

GENERAL INFORMATION:

APPLICAMT: E. I. du Pont de Nemours and Company

TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase;

FILE REFERENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 1999-01-05

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/144,783

PRIOR FILING DATE: 1999-07-20

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 FOT
CURRENT APPLICATION NUMBER: US/09/857,581
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95.8%; Pred. No. 0;
:ive 13; Mismatches
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121 IMNDLINATTVNKLRPLRTQQIRKFLRVMAQGABAQKPLDLTBELLLKWTNSTISMMVLGE 180
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT PILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR APPLICATION NUMBER: 60/114,783
PRIOR APPLICATION NUMBER: 60/126,094
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Macrosoft Office 97
SEQ ID NOS: 66
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Pred. No. 0;
1; Mismatches
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                                                                                                                                              Score 2538;
Pred. No. 0;
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Best Local Similarity 98.6%;
Matches 492; Conservative
                                                                                                                                              Query Match
Best Local Similarity 98.4%;
Matches 491; Conservative
                       LENGTH: 499
TYPE: PRT
ORGANISM: Lens culinaris
US-09-857-581-22
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SEQ ID NO 22
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GENERAL INFORMATION:
APPLICAMTON:
APPLICAMTON:
ITILE OF INVENTION: Nucleic Acid Sequences Encoding leoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT PILING DATE: 2001-06-05
PRIOR PLIING DATE: 1999-01-27
PRIOR PLLING DATE: 1999-01-27
PRIOR PLLING DATE: 1999-01-27
PRIOR PLLING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR PLLING DATE: 1999-01-24
PRIOR PLLING DATE: 1999-09-24
PRIOR PLLING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FGSMPTVVASTPELFKLFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGFYWKFVRKL 120
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Pred. No. 0;
2; Mismatches
                  PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR PELICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 59
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                                                                                                                                                                                                                                                                                                                                                                          94.98;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.6
Matches 492; Conservative
                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-857-581-22
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APPLICANT: B. I. du Pont de Nemours and Company
APPLICANT: B. I. du Pont de Nemours and Company
TITLE OP INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REPERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 1999-01-06-05
PRIOR PELING DATE: 1999-01-27
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO S5

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                                                                                                                                                                                        AEEIRDIAREVLKIYGEYSLTDFIWPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREI
                                                                                                                                                                                                                                                                                                            241 VRRKRYGEVVEGEVSGVFLDTLLEFAEDETTEIKITKDHIKGLVVDFFSAGIDSTAVATE
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IMNDLPNATIVNKLRPLRIQQTRKFLRVMAQGABAQKPLDLTBELLKWTNSTISMMLGB
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                                                                                                                                  ABEIRDIAREVLKI FGEYSLTDFIWPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREI
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Pred. No. 0;
2; Mismatches 7; Indels
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1S-09-857-581-55
Sequence 55, Application US/09857581
GENERAL INFORMATION:
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Best Local Similarity 98.2%;
Matches 490; Conservative ;
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US-09-857-581-55
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Sequence 18, Application US/09857581
Sequence 18, Application US/09857581
SEQUENCE 11 du Pont de Nemours and Company
TITLE OF INVENTION NUCLEIC Acid Sequences Encoding Isoflavone Synthase
TITLE OF INVENTION NUMBER: US/09/857,581
CURRENT FILING DATE: 1099-01-6-05
PRIOR PELICATION NUMBER: 60/117,769
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-24
PRIOR FILING DATE: 1999-09-24
SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
TYPE: PRI
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Best Local Similarity 98.2%;
Matches 490; Conservative
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ORGANISM: Vicia villosa
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Sequence 40, Application US/09857581

Sequence 40, Application US/09857581

GENERAL INFORMATION:
APPLICAMY: E. I. dw Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT PLING DATE: 1999-01-05-05

PRIOR PLING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/147,783

PRIOR PLING DATE: 1999-07-20

PRIOR PLING DATE: 1999-07-20

PRIOR PLING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

SEQ ID NO 40
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                                                                                      421 ÖHFÖLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLGVLGPGGGILKGGDAKVSMEER
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93.6%; Score 2512; D
Best Local Similarity 97.0%; Pred. No. 0;
Matches 484; Conservative 7; Mismatches
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US-09-857-581-40
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US-09-887-581-57

US-09-887-581-57

GEQUENCE 57, Application US/09857581

GENERAL INPORMATION:

APPLICANT: E. I. du Pont de Nemours and Company

ITILE OF INVENTION:

TILLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

FILE REFERENCE: BB1339 PCT

CURRENT APPLICATION NUMBER: US/09/857,581

CURRENT FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 60/117,769

PRIOR PLILNG DATE: 1999-01-27

PRIOR PLILNG DATE: 1999-01-27

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97

FEVENTION OF SEQ ID NOS: 66
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94.0%; Score 2523; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 1; Mismatches 8; Indels
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; ORGANISM: Medicago sativa
US-09-857-581-57
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Sequence 61, Application US/09857581
GENERAL INFORMATION:
APPLICANT: B. I. dw Font de Nemours and Company
ITILE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-09-24
NUMBER OF SEO ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 66
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; Sequence 20, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TILLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
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97.6%; Pred. No. 0;
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Matches 486; Conservative
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US-09-857-581-61
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GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BB1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-24
NUMBER OF SEQ ID NOS: 66
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CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
NUMBER: 0F SEQ ID NOS: 66
SOFTWARE: Mixrosoft Office 97
SEQ ID NO 20
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Best Local Similarity 96.8
Matches 483; Conservative
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US-09-857-581-20
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILES REFERENCE: BBL339 PCT
CURRENT APPLICATION NUMBER: US/9/857,581
CURRENT APPLICATION NUMBER: 00/117,769
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR PELING DATE: 1999-01-27
PRIOR PELING DATE: 1999-01-27
PRIOR PLING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-30
SOFTHARE: Microsoft Office 97
SEQ ID NO 38
LENGTH: 498
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SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 499
                                                                                                                      Query Match
Best Local Similarity 95.8<sup>3</sup>
Matches 478, Conservative
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; ORGANISM: Trifolium repens
US-09-857-581-38
                                                  TYPE: PRT
CRGANISM: Medicago sativa
US-09-857-581-16
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US-09-857-581-38
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DB 1; Length 498;

Score 2457; Pred. No. 0;

91.6%; 95.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 LAELINNPRVLQKAREEVYSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEECEINGYVIPEGALILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQH 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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                                                                                                                                                                                                                                                                                                                          122 NDLLNATTVNKLRPLRTQQIRKFLRVMAQSAEAQKPLDVTEELLKWTNSTISMMLGEAE 181
                                                    17 HLRPTFTAKSKALRHLPNPPSPKPRLPFIGHLHLLKDKLLHYALIDLSKKHGPLFSLYFG 76
                                                                                                      61
                                                                                                      2 HERPTPSAISKALRHLPNPPSPRPRLPFIGHLHLLKDKLLHYAPIDLSKKHGPLFSLSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAG
                                                                                                                                                                                                                                                                                                                                                                                                                        EIRDIAREVLKIFGEYSLTDFIWPLKYLKVGKYEKRIDDILNKFDPVVERVIKKRRIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEECEINGYVIPEGALVLFNVWQVGRDPKXWDRPSESRPERFLETGAEGEAGPLDLKGQH
  Gaps
  .;
0
  12; Indels
  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March 1, 2004, 07:04:40 Job time : 3 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTVPRAHSLVCVPLARI 498
  474; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        197
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LEFAEDETWEIKITKOHIKGLVVDFFSAGTDSTADAPTEWALAELINDFKVLEKAREV
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GVNLATSGMATLLASLIQCFDLQVLGPQQILKGGDAXVSMEERAGLTVPRAHSLVCV
                                                                                                                                                                                                                                                                                                                                                                                                     ÍGHLHILKDKLLHYALIDLSKKHGPLFSLYFGSMPTVVASTPELFKLFLGTHEATSFN
TRFQTSAIRRLTYDSSVAMVPFGPYWKFVRKLIMNDLLNATTVNKLRPLRTQQIRKFL
RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 ATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCCACACCCACTGCAAAATCAAAAGCACT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 TCGCCATCTCCCAAACCCAACAGCCAAAGCCTCGTCTTCCCTTCATAGGACACCTTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 CAAGCICTTCCTCCAAACGCAGCGAACTTCCTTCAACACAAGGTTCCAAAGCTCAGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CYP93Clv2"
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AF022462; causes change of T to I (aa 156)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ATTGGTTTTTGGCTCTGTTTCTGCACTTGCGTCCCACACCCACAAAATCAAAAGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 TCGCCATCTCCCAAACCCACCAAGCCCAAAGCCTCGTCTTCCCTTCATAGGACACCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 rererradadadadaderrerecaeracecaereareacererecaecerecadadadaderee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 CAAGCTCTTCCTCCAAACGCACGAGGCAACTTCCTTCAACACAAGGTTCCAAACCTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AGCAAAGATCAAACCAAAGCACGAGAACACACGATGTTGCTTGAACTTGCACTTGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AGCAAAGATCAAACCAAAGACGAGAACACGATGTTGCTTGAACTTGCACTTGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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Pred. No. 0;
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l. .1722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CYP93Clv2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="CYP93Clv2"
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                                                                                                                                                   36. .1601
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Best Local Similarity 99.1
Matches 1704; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
Direct Submission
Submitted (17-Max-1999) Flant Biology, Noble Foundation, 2510 Sam
Noble Pkwy, Ardmore, OK 73402, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION: AF135484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                 (without alignments)
6.282 Million cell updates/sec
                                                                                                                                                                                                                                                                                                      1824
1 GGAAAATTAGCCTCACAAAA.......TAAACTATCAATCCTTATAT 1824
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Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
Molecular characterization of the enzyme catalyzing the aryl
migration reaction of isoflavonoid biosynthesis in soybean
Arch. Biochem. Biophys. 367 (1), 146-150 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                        February 26, 2004, 16:55:28; Search time 1 Seconds
                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries
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length: 2000000000
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Match Length DB
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                                                 Copyright
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1 1685.9

No. Result

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL

FEATURES

DEFINITION

ACCESSION

RESULT 1 AF135484 LOCUS

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Minimum DB Maximum DB

Database :

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

1;

79 61 199

121

259 241 319

Qy 1460 CTTCGACTTGCAAGTG	Oy 1520 TAGCATGGAAGAGAGA 	1580	1631 ATCATATAT 	Oy 1691 ACTACTTTTATCAA DD 1682 ATCTACTTTTATCAA	Search completed: February 26, Job time : 2 secs												
380 CATAAGACGCCTCACCTATGATAGCTCAGTGGCCATGGTTCCCTTCGGACCTTACTGGAA 439 	440 GTTCGTGAGGAAGCTCATCATGAACGACCTTCCCAACGCCACCGTGTAAACAAGTTGAG 499 422 GTTCGTGAAGCAAGCTCATCATGAACGACCTTCTCAACGCCACCACTGTAAACAAGTTGAG 481	GCCTTTGAGGACCCAACAGACCGCAAGTTCCTTAGGGTTATGGCCCAAGGCGCAGAGGCGCAGAGGCCCAAGAGCGCAAGAGCCCAACAGAAGTCCTTAGAGTTATGGCCCAAGGCGCAAGTCCAACAGAGGCCAACAGAAGTCCTTTGAGGTTATGGCCCAAAGGCGCAAGTCCTTAGAGGTTATGGCCCAAAGGCGCAAGTCCTTAGAGGTTATGGCCCAAAGGCGCAAGAGGC	560 ACAGAAGCCCCTTGACTGACGAGGGCTTCTGAAATGGACCAACAGCACCATCTCCAT 619 	620 GATGATGCTCGGCGAGGCTGAGGAGATCAGAGACATCGCTCGC	680 TGGGGAATACAGCCTCACTGACTTCATCTGAGCGATTGAAGCATCTCAAGGTTGGAAAGTA 739 	740 TGAGAAGATCGACGACATCTTGAACAAGTTCGACCCTGTCGTTGAAAGGGTCATCAA 799 	800 GAAGCGCCGTGAGAATCGTCAGGAGGAGAAGAAGGAGAGGTTGTTGAGGGTGAGGTCAG 859 	860 CGGGGTTTTCCTTGACACTTTGCTTGAATTCGCTGAGGATGAGACCATGGAGATCAAAAT 919 	920 CACCAAGGACCACATCGAGGTCTTGTTGTCGACTTTTTCTCGGCAGGAACAGACTCCAC 979	980 AGCGGTGGCAACACAGAGTGGGCATTGGCAQAACTCATCAACAATCCTAAGGTGTTGGAAAA 1039 	1040 GGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAGGACAACTTGTGGACGAAGTTGACAC 1099 	1100 TCAAAACCTTCCTTACATTAGAGCAATCCTGAAGGAGACATTCCGCATGCACCGCCCACT 1159 	1160 CCCAGTGGTCAAAGAAAGTGCACAGAAGAGTGTGAGATTAATGGATATGTGATCCCAGA 1219 	1220 GGGAGCAITGAITCTCTCAAIGTAIGGCAAGIAGGAAGAGACCCCAAAIACIGGGACAG 1279 	1280 ACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAGACAGGGGCTGAAGGGGAAGCAGGGCC 1339 	1340 TCTTGATCTTAGGGGACAACATTTCAACTTCTCCCATTTGGGTCTGGGAGGAGAATGTG 1399 	1400 CCCTGGAGTCAATCTGGCTACTTCGGGAATGCCAACACTTCTTGCATCTTTTTTCAGTG 1459 
γς Ω	& 8	상 원	QV Db	8 8	ଦୁ କୁପ	9 9	oy D	Q Dp	දුරු පු	QJ Dp	Qy Dp	çy Qo	ç da	y do	Qy Dp	Qy Dp	ව රා